

OM nucleic - nucleic search, using sw model

Run on: April 3, 2004, 00:09:01 ; Search time 3852.78 Seconds
(without alignments)
16863.481 Million cell updates/sec

Title: US-10-030-269A-1
Perfect score: 1499
Sequence: 1 gcggctgcagcggctgtta.....taaatgtttttattctctc 1499

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: gb_ba:**
- 2: gb_htg:**
- 3: gb_in:**
- 4: gb_on:**
- 5: gb_ov:**
- 6: gb_pat:**
- 7: gb_ph:**
- 8: gb_pl:**
- 9: gb_pr:**
- 10: gb_ro:**
- 11: gb_sts:**
- 12: gb_sy:**
- 13: gb_un:**
- 14: gb_vi:**
- 15: em_ba:**
- 16: em_fun:**
- 17: em_hum:**
- 18: em_in:**
- 19: em_mu:**
- 20: em_om:**
- 21: em_or:**
- 22: em_ov:**
- 23: em_pat:**
- 24: em_ph:**
- 25: em_pl:**
- 26: em_ro:**
- 27: em_sts:**
- 28: em_un:**
- 29: em_vi:**
- 30: em_htg_hum:**
- 31: em_htg_inv:**
- 32: em_htg_other:**
- 33: em_htg_mus:**

- 34: em_htg_pln:**
- 35: em_htg_rod:**
- 36: em_htg_man:**
- 37: em_htg_vrt:**
- 38: em_sy:**
- 39: em_htgo_hum:**
- 40: em_htgo_mus:**
- 41: em_htgo_other:**

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1499	100.0	1499	6	AX136089	AX136089 Sequence
2	1499	100.0	1499	6	BD093294	BD093294 Amyloid b
3	1499	100.0	1499	6	BD123497	BD123497 Secretary
4	1499	100.0	1499	9	AK075335	AK075335 Homo sapi
5	1494.2	99.7	1504	6	BD063628	BD063628 Human pro
6	1483.8	99.0	1519	6	BD186179	BD186179 STAT6 act
7	1481.6	98.8	1533	9	BC001106	BC001106 Homo sapi
8	1480	98.7	1562	6	BD170687	BD170687 NF-kappa
9	1478	98.6	1503	6	BD186178	BD186178 STAT6 act
10	1475	98.4	1552	6	AX086058	AX086058 Sequence
11	1475	98.4	1552	9	HS0801574	AX136600 Homo sapi
12	1474.4	98.4	1552	9	AK091726	AK091726 Homo sapi
13	1473.6	98.3	1564	6	AX376178	AX376178 Sequence
14	1473.6	98.3	1564	6	AX696999	AX696999 Sequence
15	1473.6	98.3	1564	9	AY359012	AY359012 Homo sapi
16	1472	98.2	1544	9	AK054883	AK054883 Homo sapi
17	1469.6	98.0	1571	6	AR400559	AR400559 Sequence
18	1469.6	98.0	1571	6	AX013063	AX013063 Sequence
19	1469.6	98.0	1571	6	BD206244	BD206244 Human nuc
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28	548.8	36.6	552	9	AB013909	AB013909 Homo sapi
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31	544.4	36.3	575	6	BD123693	BD123693 Secretary
32	422.4	28.2	446	6	AR424082	AR424082 Sequence
33	422.4	28.2	446	6	BD119635	BD119635 EST and e
34	397.4	26.5	542	6	AR412344	AR412344 Sequence
35	397.4	26.5	542	6	BD108097	BD108097 EST and e
36	380.4	25.4	404	6	AR413779	AR413779 Sequence
37	380.4	25.4	404	6	BD109332	BD109332 EST and e
38	348.8	23.3	407	6	AX884371	AX884371 Sequence
39	348.8	23.3	407	6	BD023981	BD023981 Sequence
40	292.2	19.3	2072	9	BC045338	BC045338 Danio rer
41	282.4	18.8	411	11	G23808	G23808 human STS W
42	274	18.3	277	11	G21487	G21487 human STS W
43	265.2	17.7	292	6	BD060681	BD060681 Secreted
44	259.6	17.3	287	6	AX156250	AX156250 Sequence
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ALIGNMENTS

RESULT 1
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 DEFINITION
 AX136089
 AX136089
 VERSION
 AX136089.1 GI:14272497
 KEYWORDS
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1
 Oka,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and
 Hayashi,K.
 Secretory protein or membrane protein
 Patent: EP 1067182-A 11 10-JAN-2001;
 Helix Research Institute (JP)
 FEATURES
 Location/Qualifiers
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ORIGIN

Query Match 100.0%; Score 1499; DB 6; Length 1499;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 GGGGCTGAGCGGGCTTGTAGGTGTCGGGCTTGGCTGGCCAGCAAGCTTGATAGCATG 60
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 Db 61 AAGCTCTTATCTTTGGTGGCGGTGGTGGGCTTGGCTGGCCAGCAAGCTTGATAGCATG 120
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 Db 121 AAGAGTCTGAGATATCCGGTGCATATGATCTCTCCACCTTATAGAAACATCAGTGGG 180
 Qy 181 CATATTACACCAAGATGTATCCAGAGGACTGCACTGGCTGCTGAGTGGAGCC 240
 Db 181 CATATTACACCAAGATGTATCCAGAGGACTGCACTGGCTGCTGAGTGGAGCC 240
 Qy 241 ATGCCAGTGGCTGGCCATGAGCTGGAGGGCTACTGGCTGCTGGAGAGTGCAGGTACGAG 300
 Db 241 ATGCCAGTGGCTGGCCATGAGCTGGAGGGCTACTGGCTGCTGGAGAGTGCAGGTACGAG 300

Qy 301 GAGGCGAGACCCACCACTCAGGTCACTATTGTGTCATCTACCTGTCCGTGGTGGTGGC 360
 Db 301 GAGGCGAGACCCACCACTCAGGTCACTATTGTGTCATCTACCTGTCCGTGGTGGTGGC 360
 Qy 361 CTGTTGCTCTACATGGCTTCTCTGATGCTGGTGGACCTCTGATCCGAAAGCCGATGCA 420
 Db 361 CTGTTGCTCTACATGGCTTCTCTGATGCTGGTGGACCTCTGATCCGAAAGCCGATGCA 420
 Qy 421 TACACTGAGCAACTGCAATGAGGAGGAGATGAGGATGCTGCTCTATGCGAGAGCT 480
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 Qy 541 CAGCGGTGGAAGCTCGAGTGCAGGAGCAGGAGACAGTCTTCGATCGGCAAGATG 600
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 Qy 601 CTCAGCTAGATGGGCTGGTGGTGGGTCAAGGCCCCACACCATGGCTGCCAGCTCC 660
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 Db 661 AGGCTGGACAAAGCAGGGGGCTACTTCTCCCTCCCTCGGTTCCAGTCTTCCCTTAA 720
 Qy 721 GCGTGGCATTTTTCCTCTCTCCCTAAGTTCAGAAATGTTGACTTGGCTATTTGA 780
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 Qy 841 GGNATGGGAAGCAGGCGCAAGAGGGAATGAGACATTCCAGGCGGCTCAGAGTGGATG 900
 Db 841 GGNATGGGAAGCAGGCGCAAGAGGGAATGAGACATTCCAGGCGGCTCAGAGTGGATG 900
 Qy 901 CGATCTGTCTCTCTGGCTCCACTCTTGGCGGCTTCCAGCTCTGAGTCTTGGGAATGTG 960
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 Db 1081 CAGCGCTCAACCCAGCCCAAGCTCCAGGCTCAGGAGAGCTCTGATGGAGAGCTGGG 1140
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 Db 1141 CCGCTGAGCGGCACTGGGCTCTCAGGGTGCACCTGGAAGCTGTGTCGTGTCCTGTG 1200
 Qy 1201 CACTTCTGCACTGGGAGTGGAGTGCACATGCATCTGCTGCCGGTCCCTCCACTG 1260
 Db 1201 CACTTCTGCACTGGGAGTGGAGTGCACATGCATCTGCTGCCGGTCCCTCCACTG 1260

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	Dd	1261	CCCCCCCCCCCCCCCCCC	
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	Yy	1321	GTCGGTTGGACAACTGAGACTCGAGGCTGAGCGTGAGATCTGACACACAGACCCCTGTA	1380
	Dd	1321	GTGCGTGTGGAACTGAGACTCGAGGCTGAGCGTGAGATCTGACACACAGACCCCTGTA	1380
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	Yy	1441	CTTGCTTAGAGHTGTGTAAATCATAGAGAACATCAATTAATTTGTTTTATTCTCTC	1499
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LOCUS			Amyloid beta aglilation regulatory factor.	
DEFINITION		B093294		
ACCESSION		B093294		
VERSION		B093294.1	GI:22638882	
KEYWORDS		WO 0104299-A/1.		
SOURCE		Homo sapiens		
ORGANISM		Homo sapiens		
REFERENCE		1 (bases 1 to 1499)		
AUTHORS		Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Yamazaki,M., Sato,S., Arakawa,H. and Morita,M.		
TITLE		Amyloid beta aglilation regulatory factor		
JOURNAL		Patent: WO 0104299-A 1 18-JAN-2001;		
		HELIX RESEARCH INSTITUTE,TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,		
		YURI KAWAI,MAYAKO YAMAZAKI,SUSUMU SATO,HIROYUKI ARAKAWA, MASAHICO MORITA		
COMMENT		CS Homo sapiens (human)		
		PN WO 0104299-A/1		
		PD 18-JAN-2001		
		PF 06-JUL-2000 WO 2000/P004515		
		PR 08-JUL-1999 JP 99P 194179,18-OCT-1999 US 60/159586 PI		
		TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA, YURI KAWAI,MAYAKO PI		
		YAMAZAKI,		
		PI SUSUMU SATO,HIROYUKI ARAKAWA,MASAHICO MORITA		
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		A61K31/711.		
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RESULT 3

BD123497

LOCUS

DEFINITION

SECRETORY protein or membrane protein.

ACCESSION

BD123497

VERSION

BD123497.1 GI:23218442

KEYWORDS

JP 2002017376-A/6.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 1499)

Patent: JP 2002017376-A 6 22-JAN-2002;

HELIX RESEARCH INSTITUTE

OS Homo sapiens (human)

PN JP 2002017376-A/6

PD 22-JAN-2002

PF 07-JUL-2000 JP 2000253173

PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,YURI KAWAI,TOMOYASU

PI SUGIYAMA,

PI KOJI HAYASHI

PC

Cl2N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC

10, Cl2P21/02,C12Q1/68//C12P21/08,C12N15/00,C12N5/00 CC

Secretory protein or membrane protein

FT Key Location/Qualifiers

FT CDS Location/Qualifiers

source

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Best Local Similarity 100.0%; Pred. No. 0;

Matches 1499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 181 CATATTACACACCAAGATATATCCAGAGGAGCTGCAACTGCTGCAAGCTGTGGAGGCC 240

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QY 241 ATGCCAGTGTCTGGCCATGAGCTGGAGGCTACTGCTGCTGTGGAGTGGAGTGGAG 300

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Db 301 GAGGCGACACCAACCATCAAGGTCAATTTGTCACTACTGTCTGCTGTGGGTGGTGGC 360

QY 361 CTGTTGCTCTACATGGCTTCTGATGCTGGTGGAGCCCTCTGATCCGAAAGCCGATGCA 420

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QY 421 TACACTGAGCAACTGCAATGAGGAGGAGATGAGATGCTGCTCTATGCGACAGCT 480

Db 421 TACACTGAGCAACTGCAATGAGGAGGAGATGAGATGCTGCTCTATGCGACAGCT 480

QY 481 GCTGCATCCCTCGGGGGACCCCGAGCAACACAGTCTCTGAGAGCTGTGGAAGTGGCCAG 540

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QY 541 CAGCGGTGGAAGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600

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D _b	1381	TGG GTT GCG CTT GTG TCC CTT GAC TCT GGT TCC CAG TGT GCG AT GAG GAG GAA AAT TTT GTC CTT	1440
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D _b	1441	CTT GCT CTT AGA GGT TGT GTG TAA TCA GGA GGC CCA TTA TAA AAT TGT TTT ATT CTT C	1499

RESULT 5	
B063628	LOCUS
B063628	1504 bp DNA linear PAT 27-AUG-2002
DEFINITION	Human proteins having transmembrane domains and DNAs encoding these proteins.
ACCESSION	B063628
VERSION	B063628.1 GI:22609231
KEYWORDS	JP 2001508407-A/43.
SOURCE	Homo sapiens (human)

REFERENCE 1 (bases 1 to 1504)

AUTHORS Ato, S., Sekine, S., Kanda, T., and Kobayashi, H.

TITLE Human proteins having transmembrane domains and DNAs encoding these proteins

JOURNAL
Patent: JP 2001508407-A 43 26-JUN-2001;
Filing

SAGAMI CHEMICAL RESEARCH CENTER, PROTEGENE INC

COMMENT	OS	Homo sapiens (human)	PN	JP 2001508407-A/43

PD 26-JUN-2001

PF 07-NOV-1997 JP 1998522374

PR	13-NOV-1996 JP	8/301429
PI	SEISHT KATO SHINGO	SEKTE- TOMOKO
		KIMURA- MT DORI
		KOBAYASHI PC

C12N15/12, C07K14/705, C12N5/10, C12N15/57, C12N9/48, C12N9/14, PC

C12N15/55

CC Strandedness: Double;
CC Topology: Linear;

CO	Category: Linear	Key	Location/Qualifiers
FH			

FT	CDS
63.	.614.

FEATURES	Location/Qualifiers
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Query Match 99.7%; Score 1494.2; DB 6; Length 1504;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1496; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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[illegible]

[illegible]

RESULT 6	BD186179	LOCUS	1519 bp	DNA	linear	PAT 17-JUN-2003
DEFINITION	BD186179	STAT6 activating gene.				
ACCESSION	BD186179					
VERSION	BD186179.1	GI:31878379				
KEYWORDS	WO 02096943-A/48.					
SOURCE	WO 02096943-A/48.					
ORGANISM	Homio sapiens					
	Human					
REFERENCE	Bukaryorta;	Metazoa:	Chordata:	Craniata:	Vertebrata:	Euteleostomi;
AUTHORS	Mammalia;	Eutheria;	Primates;	Catarrhini;	Hominidae;	Homo.
1	(Bases 1 to 1519)					
AUTHORS	Honda,G.,	Matsuda,A.,	Muramatsu,S.	and Ishizawa,K.		
TITLE	STAT6 activating gene					
JOURNAL	Patent: WO 02096943-A 48	05-DEC-2002;				
	ASahi Kasei Corp,	Goichi Honda,	Akio Matsuda,	Shuji Muramatsu,	Kenya	
	Ishizawa					
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QY	241	ATGCCAGTGCCTGGCCATGAAGTGGAGGCGTAACTGGCTGGTGGAGGTGCAGGTACGAG	300
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ORGANISM Homo sapiens
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 REFERENCE 1 (bases 1 to 1533)
 AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
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 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Butterfield, Y.S., Krzywicki, M.I., Skalska, U., Smalios, D.E.,
 Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
 TITLE Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 MEDLINE 22388257
 PUBMED 12477932
 REFERENCE 2 (bases 1 to 1533)
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (11-DEC-2000) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT On Aug 19, 2003 this sequence version replaced gi:12654544.
 Contact: MGC help desk
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: DCTD/BTP
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
 contact: amadansystemsbiology.org
 Anup Madan, Jessica Fahey, Erin Helton, Mark Kettman, Anuradha
 Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
 Clone distribution: MGC clone distribution information can be found
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 AUTHORS Honda, G., Matsuda, A., Muramatsu, S. and Ishizawa, K.
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 ISHIZAWA
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Db	1344	CAGACGCTGGGCTTGGAAATGAGACTCGAGGCTGAGGCTGGAATCTGACACACGACCC	1403
QY	1375	TGTACTTGGGTTGCTCTTGTCCCTGAACTCTGTACACGATGCATCGAGAGAAATTT	1434
Db	1404	TGTACTTGGGTTGCTCTTGTCCCTGAACTCTGTACACGATGCATCGAGAGAAATTT	1463
QY	1435	TGTCTCTTCTTAGAGTGTGTGTAATCAGAGAGCCATCAATAATTTATTTTATTT	1494
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QY	1495	CTCTC 1499	
Db	1524	CTCTC 1528	
RESULT 11			
LOCUS	HSN01574	1552 bp	linear PRI 20-MAR-2002
DEFINITION	Homo sapiens mRNA; cDNA DKFp56411216 (from clone DKFp5641216); complete cds.		
ACCESSION	AL136600		
VERSION	AL136600.1	GI:13276700	
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
REFERENCE			
AUTHORS	Blum,H., Bauersachs,S., Mewes,H.W., Gassenhuber,J. and Wiemann,S.		
TITLE	Direct Submission		
JOURNAL	Submitted (12-MAR-2002) MIPS, Am Klopferstutz 18a, D-82152 Martinsried, GERMANY		
COMMENT	Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by IMU (Ludwig Maximilians University, Munich/Germany) within the cDNA sequencing consortium of the German		

Genome Project.
This clone (DKFZp564I1216) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de Further
information about the clone and the sequencing project is available
at <http://mips.gsf.de/proj/cDNA/>.
Location/Qualifiers

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QY 1 CGCGCTGCAGCGGCTTTAGTGTCCGGCTTTGCTGGCCGACGAAGCCTGATAGCATG 60
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DB 84 AAGCTCTATCTTTGGTGGCGTGTGGTGGTGTGGTGGTGTGGTGGTGTGGTGGT 143
QY 121 AAGAGTTCTGAAGATATCCGGTGCATATGCTGTCCACCTTATAGAAACATCATGGG 180
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DB 204 CACATTACACAGAGATATATCCAGAGAGACTGTGTAGCAACTGCTGCGAGTGTG 263
QY 235 GAGCCATGCGAGTGTGCGCATGACGTGGAGGCTACTGCGTGTGGAGTGCAGG 294
DB 264 GAGCCATGCGAGTGTGCGCATGACGTGGAGGCTACTGCGTGTGGAGTGCAGG 323

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QY 355 GGTGCCCTGTGCTCTACATGGCCCTTCTGATGCTGGTGGACCTCTGATCCGAAAGCG 414
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QY 475 GCAGCTGCTGATTCCTCGGGGAGCCCGAGCAACACAGTCTCTGGAGGCTGTGAGAGT 534
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DB 564 GCCACAGACGGTGGAAAGCTTCAGAGTGCAGGAGCAGCGGAGACAGTCTTCGATCGGCAC 623
QY 595 AAGATGCTCAGCTAGATGGGCTGCTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 654
DB 624 AAGATGCTCAGCTAGATGGGCTGCTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 683
QY 655 GCTTCCAGGCTGCAGAGAGCAGGGGCTACTTCTCCCTTCCCTCGSTTCCAGTCTCCCT 714
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Best Local Similarity 99.6%; Pred. No. 0;
Matches 1478; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 76 GTGGGCGTGTGGGTTTGTGCCCCGAAAGAGCTGATAGCAATGAAGCTCTTATCTTTG 135
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QY 136 ATCCGGTGCATATGCATCTGTCCACCTTATAGAAACATCAGTGGGCAATTTACAGCAG 195
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QY 196 AATGTATCCAGAGAGAGCTGCAACTGCTGCACTGTGTGAGGCCCATGCGAGTGCCTGGC 255
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QY 256 CATGAGGTGAGAGGCTTACTGCTGTGTGGAGTGCAGGTGAGAGAGGCGAGAGCCAGC 315
DB 716 CATGAGGTGAGAGGCTTACTGCTGTGTGGAGTGCAGGTGAGAGAGGCGAGAGCCAGC 775

QY 316 ACCATCAAGTGCATATGTCATCTACCTGCTGGTGTGGTGTGGTGTGGTGTGGTGTGG 375
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QY 376 GCCTTCCTGATGCTGTGTGGAGCTCTGATCCGAAAGCGGAGTGCATACATGAGCAATG 435
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QY 436 CACATGAGAGAGAGAGTGTGATGCTGTGTGGAGTGCAGGTGAGAGAGGCGAGAGCCAG 495
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QY 496 GGACCCGAGCAACACAGCTCTGGAGGTGTGGAGGTGTGGAGGTGTGGAGGTGTGGAGGTG 555
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QY 556 CAGGTGCAGAGAGAGAGTGTGATGCTGTGTGGAGTGCAGGTGAGAGAGGCGAGAGCCAG 615
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QY 616 TGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG 675
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QY 1495 CTCTC 1499
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LOCUS AK091726 1959 bp mRNA linear PRI 15-JUL-2002
DEFINITION Homo sapiens cDNA FLJ34407 fls, clone HEART1000173.
ACCESSION AK091726
VERSION AK091726.1 GI:21750165
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Oshima,A., Takahashi-Fujii,A., Tanase,T., Inose,N., Takeuchi,K.,
Arita,M., Mueshino,K., Yuuki,H., Hara,H., Sugiyama,T., Irie,R.,
Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y.,
Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H.,
Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K.,
Wagatsuma,M., Murakawa,K., Kanehori,K., Sugiyama,A., Kawakami,B.,
Suzuki,Y., Sugano,S., Nagatani,K., Masuho,Y., Nagai,K. and
Isogai,T.
TITLE NEO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1959)
AUTHORS Isogai,T. and Yamamoto,J.
TITLE Direct Submission
JOURNAL Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kanetani, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.
FEATURES
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TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same
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Genentech, Inc. (US)
FEATURES Location/Qualifiers
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ORIGIN

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Best Local Similarity 99.7%; Pred. No. 0;
Matches 1476; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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RESULT 13

AX376178
LOCUS AX376178 1564 bp DNA linear PAT 01-MAR-2002
DEFINITION Sequence 245 from Patent WO0168848.
ACCESSION AX376178
VERSION AX376178.1 GI:19170481

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE

1 Baker, K.P., Chen, J., Desnoyers, L., Goddard, A., Godowski, P., J.,
Gurney, A.L., Pan, J., Smith, V., Watanabe, C.K., Wood, W.I. and
Zhang, Z.

RESULT 14							PAT 02-APR-2003
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LOCUS						DNA	linear
DEFINITION					Sequence 67 from Patent W00078961.	1564 bp	
ACCESSION					AX656999		
VERSION					AX656999.1	GI:29437995	
KEYWORDS	.						
SOURCE	Homo sapiens (human)						
ORGANISM	Homo sapiens						
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						

REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	source	ORIGIN
1	Ferrara,N., Stewart,T.A., Williams,P.M., Baker,K.P., Desnoyers,L., Eaton,D.L., Gac,W.Q., Fan,J., Botstein,D., Fong,S., Goddard,A., Godowski,P.J., Gurvey,A.L., Smith,V., Tumas,D., Wood,W.I., Grimaldi,C.J., Hillan,K.J., Paoni,N.F., Roy,M.A., and Watanabe,C.K.	Secreted and transmembrane polypeptides and nucleic acids encoding the same	Patent: WO 0078961-A 67 28-DEC-2000; Genentech Inc. (US)	Location/Qualifiers 1..1564 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"		
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QY		80	CGGTGTCCGGCTTTTGTGCTGGCCACAGCGCTGAAGCATGAAGTCTTGAGATAATCC 139			
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QY		140	GGTGCATATGCATCTGCTCCACCTTATAGAAACATCAGTGGGCAATATTACAAACCAAGT 199			
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QY		200	TATCCACAGAGGACTGCAACTGCTCCAGCTGGTGGAGCCCATGCCAGTGGCTGGCCATG 259			
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DB		384	TGAAGTGCATCATTTGTCATCTACTGCTGGTGGGTGGCTGTTGCTCTACATGGCT 443			
QY		380	TGCTGATGCTGGTGACCTCTGATCCGAAGCCGAGTGCATACACTGAGCAACTGCACA 439			
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DB		504	ATGAGGAGGAGATGAGGATGCTCGCTCTATGGCAGCAGCTCGTGCATCCCTTCGGGGGAC 563			
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Accession	AY359012.1	GI:37183141	
Version	FLI_CNA.		
Keywords	Homo sapiens (human)		
Source	Homo sapiens		
Organism	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
Reference	1 (bases 1 to 1564)		
Authors	Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J., Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B., Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E., Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S., Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C., Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V., Stinson,J., Vagts,A., Vanden,R., Watanabe,C., Wieand,D., Woods,K., Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z., Goddard,A., Wood,W.I. and Godowski,P.		
Title	The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment		
Journal	Genome Res. 13 (10), 2265-2270 (2003)		
PubMed	12975309		
Reference	2 (bases 1 to 1564)		
Authors	Clark,H.F.		
Title	Direct Submission		
Journal	Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA		
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		/clone="DNA60278"	
gene	1..1564		
		/locus_tag="UNQ631"	
CDS	122..673	/locus_tag="UNQ631"	
		/notes="PRO1248"	
		/codon_start=1	
		/product="TME9"	
		/protein_id="A0C89371.1"	
		/db_xref="GI:37183142"	
		/translation="MKLSIVAVVGVCLVFPFAFKNSEDIKCKICPYPNITSGHY NQNVGQNCCHVHEVPEHDVAVCLICRYSVERSTTIKVIVLYLSVGLAL LLYMAYIMVDPILRPFDAYTEQLHNEEDARSMAAAASIGSPRANTVLERVGA QQRWKLVQEQKRTVDRKMLS"	
ORIGIN			
Query Match	96.3%	Score 1473.6; DB 9; Length 1564;	
Best Local Similarity	99.7%	Fred. No. 0;	
Matches 1476;	Conservative 0;	Mismatches 4; Indels 0; Gaps 0;	
QY	20	AGGTGTCGGGTGTTCCTGGCCACGACGCTGATAGCATGAAGCTCTTATCTTGGTG 79	
Db	84	AGGTGTCGGGTGTTCCTGGCCACGACGCTGATAGCATGAAGCTCTTATCTTGGTG 143	
QY	80	COGTGTCGGGTGTTCCTGGTGCOCOCACGCTGAAGCCACAAAGTCTCTGAAGATATCC 139	
Db	144	CTGTGTCGGGTGTTCCTGGTGCOCOCACGCTGAAGCCACAAAGTCTCTGAAGATATCC 203	
QY	140	GGTGCMAATGATCTGTCCACCTTATAGAACATCATGTGGGCAATTTTACACCAAGATG 199	
Db	204	GGTGCMAATGATCTGTCCACCTTATAGAACATCATGTGGGCAATTTTACACCAAGATG 263	

DEFINITION

QY 200 TATCCCAAGAGGACTGCAACTGCTGCAGGTGGTGGAGGCCATGCCAGTGGCTGGCCATG 259
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Db 264 TATCCCAAGAGGACTGCAACTGCTGCAGGTGGTGGAGGCCATGCCAGTGGCTGGCCATG 323
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QY 380 TCTGTATGCTGGTGGACCTCTGATCCGAAAGGCGCGATGCATACACTGAGGCACTGCACA 439
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|||||
QY 500 CCGAGCAAAACACAGTCTCTGGAGCGGTGGCAAGGTGCCAGCAAGGCTGGAAGCTGCAGG 559
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QY 560 TGCAGGAGCGCGGAGACAGTCTTGATCGGCAACAGATGCTCAGCTAGATGGCTGGCTGGT 619
|||||
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QY 740 CTCTCCCTAACTTASAAATGTTGACTTGGCTATTTGATAGGAGGAGGAGTGG 799
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QY 800 TCTCTGATCTGTGTCTCTGGGTCTTTGGGTTGAAGGATGGGAGGAGGAGGAGGCA 859
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QY 980 CTGGTCTTCAGGAATCAGTGTCTGGGAGGAAAGCATGCCCCAGCATTCAGCATGTGT 1039
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QY 1040 CCTTTCTGAGTGGTCTTATCACACCTCCCTCCAGCCCAAGCGGCTCAGGCCAGCC 1099
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QY 1100 CCACTCCAGCCCTGAGGACAGCTCTGATGGGAGGCTGGGCGCCCTGAGCCACTGGGT 1159
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Db 1164 CCACTCCAGCCCTGAGGACAGCTCTGATGGGAGAGCTGGGCGCCCTGAGCCCACTGGGT 1223
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QY 1160 CTTCAAGGTGCATCTGGAAGCTGGTGTTCGTGTCCCTGTGCATCTTCCCACTGGGGCA 1219
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|||||
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Db 1404 TCGAGGCTGAGGCTGGATCTGAACAGCACAGCCCTGTACTTGGGTGGCTCTTGTCCCT 1463
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QY 1400 GAACTTGGTGTACCACTGCACTGGAGAGAAATTTTGTCTCTTGTCTTAGAGTGTGTG 1459
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Db 1464 GAACTTGGTGTACCACTGCACTGGAGAGAAATTTTGTCTCTTGTCTTAGAGTGTGTG 1523
|||||
QY 1460 TAAATCAAGGAAGCCATCATTAATTTGTTTATTCTCTC 1499
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Db 1524 TAAATCAAGGAAGCCATCATTAATTTGTTTATTCTCTC 1563
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Job time : 3859.98 secs

OM nucleic - nucleic search, using sw model

Run on: April 2, 2004, 21:47:00 ; Search time 375.536 Seconds
(without alignments)
16957.243 Million cell updates/sec

Title: US-10-030-269A-1
Perfect score: 1499
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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: geneseqn1990s.*
3: geneseqn2000s.*
4: geneseqn2001as.*
5: geneseqn2001bs.*
6: geneseqn2002s.*
7: geneseqn2003as.*
8: geneseqn2003bs.*
9: geneseqn2003cs.*
10: geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Nc.	Score	Query	Match	Length	DB	ID	Description
1	1499	100.0	1499	4	AAF29357			Aaf29357 Amyloid-b
2	1499	100.0	1499	5	AAF93749			Aaf93749 Human cDN
3	1494.2	99.7	1504	2	AAV49584			Aav49584 Human sto
4	1481.6	98.8	1937	5	ABV23182			Abv23182 Human pro
5	1481.4	98.8	1645	3	AAF21831			Aaf21831 Human bre
6	1480	98.7	1562	6	ABQ91986			Abq91986 Human NF-
7	1479.6	98.7	1565	3	AAA39939			Aaa39939 Human TAN
8	1475	98.4	1552	5	ABX71217			Abx71217 Human tra
9	1473.6	98.3	1564	3	AAA37041			Aaa37041 Human PRO
10	1473.6	98.3	1564	4	AAF54249			Aaf54249 DNA encod
11	1473.6	98.3	1564	4	AAS46047			Aas46047 Human DNA
12	1473.6	98.3	1564	7	ABX78650			Abx78650 Human PRO
13	1473.6	98.3	1564	7	ACA75622			Aca75622 Novel hum

14	1473.6	98.3	1564	7	ACA71102			Aca71102 Human sec
15	1473.6	98.3	1564	7	ACC87630			Acc87630 Human sec
16	1473.6	98.3	1564	7	ACC87016			Acc87016 Human sec
17	1473.6	98.3	1564	7	ACD04189			AcD04189 Human sec
18	1473.6	98.3	1564	7	ACA69520			AcA69520 cDNA enco
19	1473.6	98.3	1564	7	ACA90365			AcA90365 Novel hum
20	1473.6	98.3	1564	7	ACC89472			Acc89472 Human sec
21	1473.6	98.3	1564	7	ACA98263			AcA98263 Novel hum
22	1473.6	98.3	1564	7	ACA93905			AcA93905 Human sec
23	1473.6	98.3	1564	7	ACD15298			AcD15298 Human sec
24	1473.6	98.3	1564	7	ACD08885			AcD08885 Human sec
25	1473.6	98.3	1564	7	ACC96805			Acc96805 Human sec
26	1473.6	98.3	1564	7	ACF15526			AcF15526 Human sec
27	1473.6	98.3	1564	7	ACA72893			AcA72893 Human PRO
28	1473.6	98.3	1564	7	ACD03065			AcD03065 Novel hum
29	1473.6	98.3	1564	7	ACD01880			AcD01880 Novel hum
30	1473.6	98.3	1564	7	ACA92072			AcA92072 Novel hum
31	1473.6	98.3	1564	7	ACA89497			AcA89497 cDNA enco
32	1473.6	98.3	1564	7	ACA73507			AcA73507 Human sec
33	1473.6	98.3	1564	7	ACA05822			AcA05822 Human sec
34	1473.6	98.3	1564	7	ACA66656			AcA66656 cDNA enco
35	1473.6	98.3	1564	7	ACF20231			AcF20231 Human sec
36	1473.6	98.3	1564	7	ACF19617			AcF19617 Human sec
37	1473.6	98.3	1564	7	ACD21905			AcD21905 Human sec
38	1473.6	98.3	1564	7	ACF13070			AcF13070 Human sec
39	1473.6	98.3	1564	7	ACD25173			AcD25173 Human sec
40	1473.6	98.3	1564	7	ACF00222			AcF00222 Human sec
41	1473.6	98.3	1564	7	ACA72279			AcA72279 Novel hum
42	1473.6	98.3	1564	7	ACD04803			AcD04803 Novel hum
43	1473.6	98.3	1564	7	ACD18264			AcD18264 Human sec
44	1473.6	98.3	1564	7	ACD08271			AcD08271 Human sec
45	1473.6	98.3	1564	7	ACA88705			AcA88705 Novel hum

ALIGNMENTS

RESULT 1

AAF29357
ID AAF29357 standard; DNA; 1499 BP.
XX
AC AAF29357;
XX
XX
DI 20-APR-2001 (first entry)
XX
DE Anyloid-beta protein agglutination regulating factor DNA SEQ ID 1.
XX
KW Human; amyloid-beta protein; agglutination regulatory factor;
KW Alzheimer's disease; ds.
XX
OS Homo sapiens.
XX
FN WO200104299-A1.
XX
PD 18-JAN-2001.
XX
PF 06-JUL-2000; 2000WO-JP004515.
XX
PR 08-JUL-1999; 99JP-00194179.
PR 18-OCT-1999; 99US-0159586P.
XX
PA (HELI-) HELIX RES INST.
XX

PI Ota T, Isozaki T, Nishikawa T, Kawai Y, Yamazaki M, Satoh S;
PI Arakawa H, Morita M;
XX WPI; 2001-138347/14.
DR P-PSDB; A249767.
XX
PT Polynucleotide encoding amyloid-beta protein agglutination-controlling
PT factor, useful for inhibiting or promoting agglutination or sedimentation
PT of amyloid-beta protein and in diagnosis and screening drugs for
PT Alzheimer's disease.
XX
PS Claim 1; Page 43-45; 72pp; Japanese.
XX
CC This invention relates to polynucleotides AAF29357 ~ AAF29361 which
CC encode proteins AAB49767 ~ AAB49771. The proteins inhibit or promote the
CC agglutination of amyloid beta protein. The protein and polynucleotide
CC sequences are useful in the diagnosis of Alzheimer's disease. They are
CC also useful for screening drugs which are useful for treating Alzheimer's
CC disease
XX
SQ Sequence 1499 BP; 293 A; 408 C; 430 G; 368 T; 0 U; 0 Other;
Query Match 100.0%; Score 1499; DB 4; Length 1499;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCGGCTGACGCGGGCTTTAGGTGTCCGGCTTTGCTGGCCGACGAAAGCTGATGATG 60
DB 1 GCGGCTGACGCGGGCTTTAGGTGTCCGGCTTTGCTGGCCGACGAAAGCTGATGATG 60
QY 61 AAGCTCTATCTTTGGTGGCGGTGCGGTGTTGCTGGTGGCCGACGAAAGCTGATGATG 120
DB 61 AAGCTCTATCTTTGGTGGCGGTGCGGTGTTGCTGGTGGCCGACGAAAGCTGATGATG 120
QY 121 AAGGTTCTGAAGATTCGGTGCATATGCAATGCTGTCCGCTTATGAACATCATGATG 180
DB 121 AAGGTTCTGAAGATTCGGTGCATATGCAATGCTGTCCGCTTATGAACATCATGATG 180
QY 181 CATATTTACACCAAGAAATGTATCCAGAAAGAACTGCAACTGGCTGCAAGTACGAG 240
DB 181 CATATTTACACCAAGAAATGTATCCAGAAAGAACTGCAACTGGCTGCAAGTACGAG 240
QY 241 ATGCCAGTGCCTGCGCATGAGTGGGCGTACTGCTGCTGTGGAGTGCAGTACGAG 300
DB 241 ATGCCAGTGCCTGCGCATGAGTGGGCGTACTGCTGCTGTGGAGTGCAGTACGAG 300
QY 301 GAGCGACGACCAACCAACCAATCAAGTCAATGATGATGATGATGATGATGATGATG 360
DB 301 GAGCGACGACCAACCAACCAATCAAGTCAATGATGATGATGATGATGATGATGATG 360
QY 361 CTGTTGCTTACATGCGCTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
DB 361 CTGTTGCTTACATGCGCTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
QY 421 TACACTGAGCAACTGCAATGAGGAGGATGAGGATGCTGCTGCTGCTGCTGCTGCTG 480
DB 421 TACACTGAGCAACTGCAATGAGGAGGATGAGGATGCTGCTGCTGCTGCTGCTGCTG 480
QY 481 GCTGCATCCCTCGGGGACCCCGAGCAACACAGTGCCTGAGAGGCTGAGAGGCTGCCAG 540
DB 481 GCTGCATCCCTCGGGGACCCCGAGCAACACAGTGCCTGAGAGGCTGAGAGGCTGCCAG 540
QY 541 CAGGGTGGAGCTGCAAGTGCAGGACGACGCGGAAGACATCTTCTGATCGGACAGATG 600

DB 541 CAGGGTGGAGCTGCAAGTGCAGGAGACGCGGAAGACAGTCTTGGATCGGACAGATG 600
QY 601 CTCAGCTAGATGAGGCTGGTGTGGTGGGTCAAGGCCCCCAACACCATGGCTGCCAGCTCC 660
DB 601 CTCAGCTAGATGAGGCTGGTGTGGTGGGTCAAGGCCCCCAACACCATGGCTGCCAGCTCC 660
QY 661 AGGCTGACAAAGCAAGGGGCTACTTCTCCCTTCCCTGGTTCAGTCTTCCCTTAA 720
DB 661 AGGCTGACAAAGCAAGGGGCTACTTCTCCCTTCCCTGGTTCAGTCTTCCCTTAA 720
QY 721 GCGTGTGGCAATTTTCTCCCTCTCCCTAAGTGTAGAAATGTGCTACTGGCTATTTGA 780
DB 721 GCGTGTGGCAATTTTCTCCCTCTCCCTAAGTGTAGAAATGTGCTACTGGCTATTTGA 780
QY 781 TTAGGGAAGAGGATGTGGTCTCTGATCTGTGTCTTCTTGGGTCTTGGGTGTAAG 840
DB 781 TTAGGGAAGAGGATGTGGTCTCTGATCTGTGTCTTCTTGGGTCTTGGGTGTAAG 840
QY 841 GATGGGGAAGGACGACGAGGGAATGGAGACATTCAGGGGCTCAGAGTGGATG 900
DB 841 GATGGGGAAGGACGACGAGGGAATGGAGACATTCAGGGGCTCAGAGTGGATG 900
QY 901 CGATCTGTCTCTCCCTGGCTCCACTCTTGGCCCTTCCAGCTCTGAGTCTTGGGAATGTG 960
DB 901 CGATCTGTCTCTCCCTGGCTCCACTCTTGGCCCTTCCAGCTCTGAGTCTTGGGAATGTG 960
QY 961 TTACGCTTGGAAATAAGCTGGGTCTTCAGGAATCAGTGTCTGGGGAAGGATGGC 1020
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QY 1081 CAGCGCTCAGCCGACGAGCCGACGCTCCAGGCTGAGGAGCTCTGATGGGAGAGCTGG 1140
DB 1081 CAGCGCTCAGCCGACGAGCCGACGCTCCAGGCTGAGGAGCTCTGATGGGAGAGCTGG 1140
QY 1141 CCGCTGAGCCCACTGGGTCTTCAAGGCTGCACTGGAAGCTGTGTGCTGTCCCTGTG 1200
DB 1141 CCGCTGAGCCCACTGGGTCTTCAAGGCTGCACTGGAAGCTGTGTGCTGTCCCTGTG 1200
QY 1201 CACTTCTGCACTGGGCGATGAGTGCCTGATGCTCTGCTGCTGCTGCTGCTGCTGCTG 1260
DB 1201 CACTTCTGCACTGGGCGATGAGTGCCTGATGCTCTGCTGCTGCTGCTGCTGCTGCTG 1260
QY 1261 CACTTGGGGGTCTGGGCACTCCCTCTCTCCAGTGTCCAGAGTCACTGAGGAGAGCTG 1320
DB 1261 CACTTGGGGGTCTGGGCACTCCCTCTCTCCAGTGTCCAGAGTCACTGAGGAGAGCTG 1320
QY 1321 GTGGTGGAAACATGAGACTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 1380
DB 1321 GTGGTGGAAACATGAGACTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 1380
QY 1381 TGGGTGGCTCTTGTCCCTGAACTGTGTTGACAGTGTGACAGTGTGAGGAGAAATTTGTCT 1440
DB 1381 TGGGTGGCTCTTGTCCCTGAACTGTGTTGACAGTGTGACAGTGTGAGGAGAAATTTGTCT 1440
QY 1441 CTTGTCTTAGAGTGTGTGTAATCAAGGAAGGCAATCATTAAATTTTATTCTCTC 1499
DB 1441 CTTGTCTTAGAGTGTGTGTAATCAAGGAAGGCAATCATTAAATTTTATTCTCTC 1499

RESULT 2
AAE93749
ID AAE93749 standard; cDNA; 1499 BP.

XX AAE93749;
XX
DT 23-MAY-2001 (first entry)
XX
DE Human cDNA encoding a membrane or secretory protein clone PSEC0012.
XX
KW Human; secretory protein; membrane protein; vaccine; gene therapy;
KW Rheumatoid arthritis; diabetes; ss.
XX
OS Homo sapiens.
XX
PN EP1067182-A2.
XX
PD 10-JAN-2001.
XX
PF 07-JUL-2000; 2000EP-00114090.
XX
PR 08-JUL-1999; 99JP-00194179.
PR 11-JAN-2000; 2000JP-00118775.
PR 02-MAY-2000; 2000JP-00183766.
XX
XX (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;
XX
XX WPI: 2001-093989/11.
DR P-FSDB; AAB88322.
XX
XX Nucleic acids encoding secretory proteins/membrane proteins, useful in
PT gene therapy or as candidate target molecules in drug development.
XX
XX Claim 1; SEQ ID NO 11; 609pp + Sequence Listing; English.
XX
XX This invention relates to nucleic acid sequences AAF93744 - AAF93916
CC which encode human secretory or membrane proteins represented by AAB88317
CC - AAB88419. Included in the invention are primers AAF93917 - AAF94295 and
CC AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the
CC invention. The invention also includes methods for the production of
CC antibodies directed against the proteins, and cDNA sequences, which can
CC be used in vaccines. The polynucleotide sequences can be used in gene
CC therapy. The polynucleotide sequences and the proteins they encode may be
CC used in the prevention, treatment and diagnosis of diseases associated
CC with inappropriate secretory protein/membrane protein expression. The
CC nucleic acids and complementary sequences may also be used as DNA probes
CC in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect
CC and quantitate the presence of similar nucleic acid sequences in samples.
CC They may also be used to study the expression and function of secretory
CC proteins/membrane polypeptides and their role in metabolism. The
CC polypeptides may be used as antigens in the production of antibodies
CC against them and in assays to identify modulators (agonists and
CC antagonists) of expression and activity. The antibodies and antagonists
CC may also be used as therapeutic agents to down regulate expression and
CC activity. The antibodies may also be used as diagnostic agents for
CC detecting the presence of the polypeptides in samples (e.g. by enzyme
CC linked immunosorbent assay (ELISA)). Examples of diseases which may be
CC treated include rheumatoid arthritis and diabetes
XX
XX Sequence 1499 BP; 293 A; 408 C; 430 G; 368 T; 0 U; 0 Other;

Query Match 100.0%; Score 1499; DB 5; Length 1499;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGCTGAGGGGCTTGTAGGTGTGGGCTTTGCTGGCCAGCAAGCTGATAGCATG 60
DB 1 GCGGCTGAGGGGCTTGTAGGTGTGGGCTTTGCTGGCCAGCAAGCTGATAGCATG 60

QY 61 AAGCTCTTATCTTTTGTGGCGGTGGTGGGTTTCTGGTGGCCAGCAAGCTGATAGCATG 120
DB 61 AAGCTCTTATCTTTTGTGGCGGTGGTGGGTTTCTGGTGGCCAGCAAGCTGATAGCATG 120

QY 121 AAGGTTCTGAAGATATCCGGTGCATATGCACTGTCACTTATAGAAACATCAGTGGG 180
DB 121 AAGGTTCTGAAGATATCCGGTGCATATGCACTGTCACTTATAGAAACATCAGTGGG 180

QY 181 CATATTACAAACAGATATATCCAGAAAGGACTGCACTGCTGCACGCTGGTGGAGCC 240
DB 181 CATATTACAAACAGATATATCCAGAAAGGACTGCACTGCTGCACGCTGGTGGAGCC 240

QY 241 ATGOCAGTGGCTGGCCATGAGGTGAGGCTTACTTGGCTGTGGAGTGCAGTACAG 300
DB 241 ATGOCAGTGGCTGGCCATGAGGTGAGGCTTACTTGGCTGTGGAGTGCAGTACAG 300

QY 301 GAGGCGAGCAGCACCACCAATCAAGGTTCATTTCTCACTACCTGTCCGTGGTGGC 360
DB 301 GAGGCGAGCAGCACCACCAATCAAGGTTCATTTCTCACTACCTGTCCGTGGTGGC 360

QY 361 CTGTGCTCTACATGGCTTCTGTGGAGCTTCTGATCCGAAAGCCGAGTGA 420
DB 361 CTGTGCTCTACATGGCTTCTGTGGAGCTTCTGATCCGAAAGCCGAGTGA 420

QY 421 TACACTGAGCAACTGCACATGAGAGGAGAAATGAGATGCTGCTCTATGCGACAGCT 480
DB 421 TACACTGAGCAACTGCACATGAGAGGAGAAATGAGATGCTGCTCTATGCGACAGCT 480

QY 481 GGTGCACTCCCTCGGGGACCCGAGCAGACAGCTCTGAGCTGTGGAGAGTGGCCAG 540
DB 481 GGTGCACTCCCTCGGGGACCCGAGCAGACAGCTCTGAGCTGTGGAGAGTGGCCAG 540

QY 541 CAGCGGTGGAAGCTGCAGGTGCAGGAGCAGGGAAGACAGTCTTGGATCGGCAAGATG 600
DB 541 CAGCGGTGGAAGCTGCAGGTGCAGGAGCAGGGAAGACAGTCTTGGATCGGCAAGATG 600

QY 601 CTGAGTGAATGGGCTGTGGTGTGGTGAAGGCCCAACACCATGGTGCACAGCTTC 660
DB 601 CTGAGTGAATGGGCTGTGGTGTGGTGAAGGCCCAACACCATGGTGCACAGCTTC 660

QY 661 AGGCTGGACAAAGCAGGGGCTTCTCTCCCTCCCTGGGTCCAGTCTTCCCTTAAA 720
DB 661 AGGCTGGACAAAGCAGGGGCTTCTCTCCCTCCCTGGGTCCAGTCTTCCCTTAAA 720

QY 721 GCGTGTGGCAATTTTCTCTCTCCCTTAACCTTTAGAAATGTTGACTTGGCTATTTGA 780
DB 721 GCGTGTGGCAATTTTCTCTCTCCCTTAACCTTTAGAAATGTTGACTTGGCTATTTGA 780

QY 781 TTAGGGAAGAGGATGTGCTCTGATCTGTGCTTCTGGGTCTTTGGGTGAAG 840
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QY 841 GGATGGGAGGCGCAGAGGGAATGACATTCAGAGCGGCTCAGGAGTGGATG 900
DB 841 GGATGGGAGGCGCAGAGGGAATGACATTCAGAGCGGCTCAGGAGTGGATG 900

D6	841	GGATGGGGAAGCCAGCCAGAAAGGATATGAGACATCTGAGGGGGCCTCAGAGATGGATG	900
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D6	901	CGATCTGTCTCTCTGGCTCCACATCTTGCCGCTTCCAGCTCTGAGTCTTGGGAATGTG	960
Q7	961	TTACCTTGGAAAGATAAAGCTGGGTCTTCAGGAACCTCAGTGTCTGGGAGGAAGCATGGC	1020
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Q7	1021	CCAGCATTCACATATGTCTTCTTCTGCAGTGGTCTTATCACACCTCCCTCCACGCC	1080
D6	1021	CCAGCATTCACATATGTCTTCTTCTGCAGTGGTCTTATCACACCTCCCTCCACGCC	1080
Q7	1081	CAGGGCTCAGCCOCCAGCCAGCTCCAGCCCTGAGGACGCTCTGATGGGAGAGCTGGG	1140
D6	1081	CAGGGCTCAGCCOCCAGCCAGCTCCAGCCCTGAGGACGCTCTGATGGGAGAGCTGGG	1140
Q7	1141	CCGCTTGAGCCCACTGGGTCTTCAGGTGGCACTGGAACTGGTTCGCTGTCCCTGTG	1200
D6	1141	CCGCTTGAGCCCACTGGGTCTTCAGGTGGCACTGGAACTGGTTCGCTGTCCCTGTG	1200
Q7	1201	CACCTTCCTGGCACTGGGGCACTGGAGTGCCTCATGATACTCTGCTGGCGGTCCCTCAGCTG	1260
D6	1201	CACCTTCCTGGCACTGGGGCACTGGAGTGCCTCATGATACTCTGCTGGCGGTCCCTCAGCTG	1260
Q7	1261	CACCTTGAGGGGTCTGGGCACTGCTCCTCTCCCAAGTGTCCACAGTCACTGAGCCAGAG	1320
D6	1261	CACCTTGAGGGGTCTGGGCACTGCTCCTCTCCCAAGTGTCCACAGTCACTGAGCCAGAG	1320
Q7	1321	GTGGGTGGACATGAGACTGGAGGCTGAGGCTGGATCTGAACACCAAGCCCTGTACT	1380
D6	1321	GTGGGTGGACATGAGACTGGAGGCTGAGGCTGGATCTGAACACCAAGCCCTGTACT	1380
Q7	1381	TGGGTTGGCTCTTGTCCCTGAACCTGGTGTACCACTGCATGGAGAGAAATTTTGTCT	1440
D6	1381	TGGGTTGGCTCTTGTCCCTGAACCTGGTGTACCACTGCATGGAGAGAAATTTTGTCT	1440
Q7	1441	CTTGTCTTAGAGTTGTGTGTAATCAAGGAAGCAATATAATGTTTTTATTTCTCTC	1499
D6	1441	CTTGTCTTAGAGTTGTGTGTAATCAAGGAAGCAATATAATGTTTTTATTTCTCTC	1499

RESULT 3	
AAV49584	
ID	AAV49584 standard; cDNA to mRNA; 1504 BP.
XX	
XX	AAV49584;
XX	
DT	21-Oct-1998 (first entry)
XX	
DE	Human stomach cancer cell clone HPI0297 cDNA #1.
XX	
KW	Transmembrane domain; human; nutrition; cytokine; cell proliferation;
KW	differentiation; immune system; stimulator; suppressor; regulator;
KW	hematopoiesis; activin; inhibitor; chemotactic; chemokinetic; receptor;
KW	hemostatic; thrombolytic; ligand; anti-inflammatory; tumour; ds.
XX	
CS	Homo sapiens.
XX	
XX	
Key	Location/Qualifiers
FT	63..614
CDS	/*tag= a
FT	

```

/product= "transmembrane domain containing protein"
FT XX
XX
PN PN W09821328-A2.
XX
XX PD 22-MAY-1998.
XX
XX PF 07-NOV-1997; 9TWO-JP004056.
XX
XX PA 13-NOV-1996; 96JP-00301429.
PPR (SAGA ) SAGAMI CHEM RES CENTRE.
XX (PROT-) PROTEGENE INC.
PA
XX Kato S, Sekine S, Yamaguchi T, Kobayashi M;
PI
XX WP1: 1998-297932/26..
DR P-PSDB: AAW64551.
XX
XX Human protein having transmembrane domain - useful for, e.g. research and
PT nutrition..
PT
XX Claim 4; Page 162-163; 205pp; English.
PS
XX AAIV9550-V49599 are cDNA sequences which encode human proteins containing
CC a transmembrane domain. These proteins can be used for, e.g. research and
XX nutrition, and may have cytokine and cell proliferation/differentiation,
CC immune stimulating/suppressing, haematopoiesis regulating, tissue growth,
CC activin/inhibin, chemotactic/chemokinetic, haemostatic and thrombolytic,
CC receptor/ligand, anti-inflammatory or tumour inhibition activity
SQ
XX Sequence 1504 BP; 293 A; 409 C; 431 G; 371 T; 0 U; 0 Other;

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Query Match      99.7%; Score 1494.2; DB 2; Length 1504;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1496; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

QY	1	GC	GCCTGCACGCGGGCTGTAGGTGTCCGGCTTTCTGGCCCGACGAAGCCTGATAACGATG	60
Db	6	GC	GCCTGCACGCGGGCTTGTAGGTGTCCGGCTTTCTGGCCCGACGAAGCCTGATAACGATG	65
QY	61	AA	GCCTTATCTTTTGGTGGCCGTGTCCGGGTGTTTGCTGTGCCGCCAGCTGAAGCCAAC	120
Db	66	AA	GCCTTATCTTTTGGTGGCCGTGTCCGGGTGTTTGCTGTGCCGCCAGCTGAAGCCAAC	125
QY	121	AA	GAGTTCTGAAGATCCGGTGCAAATGCATCTGTCAACCTTATAGAACATCATGTGGG	180
Db	126	AA	GAGTTCTGAAGATCCGGTGCAAATGCATCTGTCAACCTTATAGAACATCATGTGGG	185
QY	181	CA	TATTTAAACCAAGATGTATCCAGAAGCATGCACTGCCTGCACGTGTGGAGGCC	240
Db	186	CA	TATTTAAACCAAGATGTATCCAGAAGCATGCACTGCCTGCACGTGTGGAGGCC	245
QY	241	AT	GCAAGTGCCTGGCCATGACGTGGAGGCCCTACTGCCTGCTGTGGAGTGCAGGTACGAG	300
Db	246	AT	GCAAGTGCCTGGCCATGACGTGGAGGCCCTACTGCCTGCTGTGGAGTGCAGGTACGAG	305
QY	301	GAG	CGCAGCACCAACCACTCAAGAGTCATCATTTGTCACTACTGTCCGTGGTGGGTGCC	360
Db	306	GAG	CGCAGCACCAACCACTCAAGAGTCATCATTTGTCACTACTGTCCGTGGTGGGTGCC	365
QY	361	CT	GTTCATCATGGCCCTCCTGATGCTGGTGGACCTCTGATCCGAAGCCGGATGCA	420
Db	366	CT	GTTCATCATGGCCCTCCTGATGCTGGTGGACCTCTGATCCGAAGCCGGATGCA	425

Db 1326 GTCCGTTGGAACATGAGACTCGAGGCTGAGCGTTGGATCTGAACACACAGCCCTGTACT 1385
Qy 1381 TGGGTTGCTCTCTGTCCCTGACCTTCGTTGTACCGAGTGCATGGAGAGAAAATTTTGTCT 1440
Db 1386 TGGGTTGCTCTCTGTCCCTGACCTTCGTTGTACCGAGTGCATGGAGAGAAAATTTTGTCT 1445
Qy 1441 CTGTCTTAGAGTTGTGTAAATCAAGAGGACCATCAATAATGTTTATTCTCTC 1499
Db 1446 CTGTCTTAGAGTTGTGTAAATCAAGAGGACCATCAATAATGTTTATTCTCTC 1504
RESULT 4
ID ABV23182
ID ABV23182 standard; cDNA; 1937 BP.
XX AC ABV23182;
XX 16-SEP-2002 (first entry)
XX Human prostate expression marker cDNA 23173.
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX Homo sapiens.
XX WO200160860-A2.
XX 23-AUG-2001.
XX 20-FEB-2001; 2001WO-US005171.
XX 17-FEB-2000; 2000US-0183319P.
XX 16-MAR-2000; 2000US-0189862P.
XX 25-MAY-2000; 2000US-0207454P.
XX 09-JUN-2000; 2000US-0211314P.
XX 18-JUL-2000; 2000US-0219007P.
XX 13-DEC-2000; 2000US-0255281P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX Schlegel R, Endege WO, Monahan JE;
XX WPI; 2001-662795/76.
XX Novel isolated nucleic acid molecule associated with cancerous state of
XX prostate cells and correlating with presence of prostate cancer, useful
XX for detecting presence of prostate cancer, stage of prostate cancer.
XX Claim 1; Page 4163; 1175Opp; English.
XX The invention relates to an isolated nucleic acid molecule (I) comprising
XX a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the
XX specification or its complement. (I) is useful for: (a) assessing whether
XX a patient is afflicted with prostate cancer; (b) monitoring the
XX progression of prostate cancer in a patient; (c) assessing the efficacy
XX of a test compound to inhibit prostate cancer in a patient; (d) assessing
XX the efficacy of a therapy for inhibiting prostate cancer in a patient;
XX (e) selecting a composition for inhibiting prostate cancer in a patient;
XX (f) assessing the prostate cell carcinogenic potential of a compound; (g)
XX determining whether prostate cancer has metastasized in a patient; (h)
XX assessing the aggressiveness or indolence of prostate cancer in a patient
XX ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker

Qy 421 TACACTGAGCAATCTGCACATGAGAGGAGGAATGAGGATGCTGCTCTATGGCAGAGCT 480
Db 426 TACACTGAGCAATCTGCACATGAGAGGAGGAATGAGGATGCTGCTCTATGGCAGAGCT 485
Qy 451 GCTGCATCCCTCCGGGACCCCGCAGCAACACAGTCTCTGAGCGTGTGGAGGTGCCAG 540
Db 486 GCTGCATCCCTCCGGGACCCCGCAGCAACACAGTCTCTGAGCGTGTGGAGGTGCCAG 545
Qy 541 CAGCGTGGAGCTGCAAGTGCAGAGGACGAGGAGGAGGAGTCTTCGATCGGCAAGATG 600
Db 546 CAGCGTGGAGCTGCAAGTGCAGAGGACGAGGAGGAGGAGTCTTCGATCGGCAAGATG 605
Qy 601 CTCAGCTAGATGGGCTGT 660
Db 606 CTCAGCTAGATGGGCTGT 665
Qy 661 AGCTGTGCAAAAAGCAGGGGCTACTTCTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTT 720
Db 666 AGCTGTGCAAAAAGCAGGGGCTACTTCTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTT 725
Qy 721 GCTGTGGCAATTTTCT 780
Db 726 GCTGTGGCAATTTTCT 785
Qy 781 TTAGGAGAGAGGATGT 840
Db 786 TTAGGAGAGAGGATGT 845
Qy 841 GATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
Db 846 GAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 905
Qy 901 CGATCTGTCT 960
Db 906 CGATCTGTCT 965
Qy 961 TTACCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
Db 966 TTACCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1025
Qy 1021 CCAGCATTCAGCATGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1080
Db 1026 CCAGCATTCAGCATGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1085
Qy 1081 CAGGCGCTCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCA 1140
Db 1086 CAGGCGCTCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCCCAAGCC 1145
Qy 1141 CCCCCTGAGCCCACTGGGTCTTCAAGGCTGCACTGGAGCTGTGTGTGTGTGTGTGTGT 1200
Db 1146 CCCCCTGAGCCCACTGGGTCTTCAAGGCTGCACTGGAGCTGTGTGTGTGTGTGTGTGT 1205
Qy 1201 CACTTCTCGCACTGGGCGATGGAGTGGCCATGATATCTGTCTGCTGCTGCTGCTGCTG 1260
Db 1206 CACTTCTCGCACTGGGCGATGGAGTGGCCATGATATCTGTCTGCTGCTGCTGCTGCTG 1265
Qy 1261 CACTTGAAGGGTGTGGGCGATGGAGTGGCCATGATATCTGTCTGCTGCTGCTGCTGCTG 1320
Db 1266 CACTTGAAGGGTGTGGGCGATGGAGTGGCCATGATATCTGTCTGCTGCTGCTGCTGCTG 1325
Qy 1321 GTGCGTTGGACATGAGACTTCAGGCTGAGCGTGGATCTGAACACACAGCCCTGTACT 1380

XX	Sequence	1937 BP;	445 A;	510 C;	560 G;	399 T;	0 U;	23 Other;
SQ								
	Query Match	98.8%	Score	1481.6;	DB 5;	Length	1937;	
	Best Local Similarity	95.7%;	Pred. No. 0;					
	Matches 1495;	Conservative	0;	Mismatches	4;	Indels	1;	Gaps
QY	1	GCGGCTGCGAGCGGCTGTGAGTGTCCGGCTTTCCTGGCCAGCAAGCGCTGATGAACGATG	60					
DB	120	GCGGCTGCGAGCGGCTGTGAGTGTTCGGCTTTCCTGGCCAGCAAGCGCTGATGAACGATG	179					
QY	61	AAGGCTCTTATCTTTTGGTGGCCGTGGTGGGTGTTGCTGGTGGCCCGACGCTGAAGCAAC	120					
DB	180	AAGGCTCTTATCTTTTGGTGGCTGTGTGGGTGTTTGGTGGTGGCCCGACGCTGAAGCAAC	239					
QY	121	AAGAGTCTGAAGATATCGGTGCAATGCAATGCACTGTCCACCTTATAGAAGCATCACTGGG	180					
DB	240	AAGAGTCTGAAGATATCGGTGCAATGCACTGTCCACCTTATAGAAGCATCACTGGG	299					
QY	181	CATATTACACACAGATATATCCAGAGAGATGCAACTGCTGCACTGTGTGGAGGCC	240					
DB	300	CACATTACACAGATATATCCAGAGAGATGCAACTGCTGCACTGTGTGGAGGCC	359					
QY	241	ATGCGAGTGCCTGGGCATGAGGTGGAGGCTACTGGCTGGTGGAGTGCAGATGACAG	300					
DB	360	ATGCGAGTGCCTGGGCATGAGGTGGAGGCTACTGGCTGGTGGAGTGCAGATGACAG	419					
QY	301	GAGCGAGCAGCACACACATCAAGGTGATCATGTGATCATCTACTGTCGGTGGGTGGC	360					
DB	420	GAGCGAGCAGCACACACATCAAGGTGATCATGTGATCATCTACTGTCGGTGGGTGGC	479					
QY	361	CTGTTGCTCTACATGGCTTCTGTATGCTGGTGGACGCTCTGATCGGAAGCGCGATGCA	420					
DB	480	CTGTTGCTCTACATGGCTTCTGTATGCTGGTGGACGCTCTGATCGGAAGCGCGATGCA	539					
QY	421	TACACTGACGACTGCAATGAGAGGAGATGAGGATGCTGCTCTATGCGACAGCT	480					
DB	540	TACACTGACGACTGCAATGAGAGGAGATGAGGATGCTGCTCTATGCGACAGCT	599					
QY	481	GCTGCATCCCTCGGGGAGCCCGGAGCAACACATGCTGAGCGGTGTGGAAGGTGCCAG	540					
DB	600	GCTGCATCCCTCGGGGAGCCCGGAGCAACACATGCTGAGCGGTGTGGAAGGTGCCAG	659					
QY	541	CAGCGGTGGAGGTGCAGTGTGAGAGCGCGGAGAGACAGTCTTCGATCGGCAACAAGTG	600					
DB	660	CAGCGGTGGAGGTGTGAGGTGAGAGCGCGGAGAGACAGTCTTCGATCGGCAACAAGTG	719					
QY	601	CTCAGCTAGATGAGCTGGTGTGGTGGGTCAAGGCCCCAACACCATGGCTGCGAGCTCC	660					
DB	720	CTCAGCTAGATGAGCTGGTGTGGTGGGTCAAGGCCCCAACACCATGGCTGCGAGCTCC	779					
QY	661	AGGCTGGACAAAGCAGGGGCGCTACTTCTCCCTTCGCTGGTTCGAGTCTTCCTTTAAA	720					
DB	780	AGGCTGGACAAAGCAGGGGCGCTACTTCTCCCTTCGCTGGTTCGAGTCTTCCTTTAAA	839					
QY	721	GGCTGTGGCAATTTTCTCCTCTCCTCAACTTTAGAAATGTTGTACTTGGCTATTITGA	780					
DB	840	GGCTGTGGCAATTTTCTCCTCTCCTCAACTTTAGAAATGTTGTACTTGGCTATTITGA	899					
QY	781	TTAGGAAGAGGGATGTGGTCTCTGATCTCTGTTCTCTTGGGTCTTTGGGTTGAG	840					
DB	900	TTAGGAAGAGGGATGTGGTCTCTGATCTCTGTTCTCTTGGGTTGAG	959					

XX Homo sapiens.
 XX WO20055173-A1.
 XX 21-SEP-2000.
 PD 08-MAR-2000; 2000WO-US005891.
 PF 12-MAR-1999; 99US-0124270P.
 PR (HUMA-) HUMAN GENOME SCI INC.
 XX Rosen CA, Ruben SM;
 XX WPI; 2000-611515/58.
 DR P-PSDB; AAB58928.
 XX
 XX New human breast and ovarian cancer associated gene sequences and the
 PT polypeptides encoded by these genes, useful in the prevention, treatment
 PT and diagnosis of cancer, immune disorders, cardiovascular disorders and
 PT neurological diseases.
 XX
 XX Claim 1; Page 645-646; 1299pp; English.
 XX
 XX Sequences AAF21614 - AAF22031 represent DNA sequences encoding human
 CC proteins AAB58711 - AAB59128. The DNA and protein sequences are
 CC associated with breast and ovarian cancer. Included in the invention are
 CC sequences AAF22032 - AAF22040 and AAB59129 which are used in the
 CC isolation and characterisation of the DNA and protein sequences of the
 CC invention. The breast and ovarian cancer associated DNA, protein, agonist
 CC or antagonist sequences exhibit cytostatic; immunosuppressive; nootropic;
 CC neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic;
 CC antiinflammatory; antitumor; anticonvulsant; antibacterial;
 CC antifungal; antiparasitic and cardiant activity. The polynucleotide and
 CC protein sequences are used in the diagnosis of cancer, particularly
 CC breast and ovarian cancer. The nucleic acid sequences, proteins, agonists
 CC and agonists may also be used in the diagnosis, prevention and treatment
 CC of immune disorders e.g. Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
 CC cardiovascular disorders such as myocardial ischaemias; wound healing;
 CC neurological diseases such as cerebral anoxia and epilepsy; and
 CC infectious diseases
 XX
 XX Sequence 1645 BP; 400 A; 419 C; 448 G; 374 T; 0 U; 4 Other;

Query Match 98.8%; Score 1481.4; DB 3; Length 1645;
 Best Local Similarity 99.5%; Pred. No. 0;
 Matches 1493; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

QY 1 GCGGCTGCAGCGGGCTTGTAGGTGTCCGGCTTGTGCTGGCCAGACAGCCTGATAGCATG 60
 DB 39 GCGGCTGCAGCGGGCTTGTAGGTGTCCGGCTTGTGCTGGCCAGACAGCCTGATAGCATG 98
 QY 61 AGCTCTTATCTTGTGGCGGTGTGGGTGTTTGGTGTCCCGCAGCTGAGCCAC 120
 DB 99 AGCTCTTATCTTGTGGGTGTGGGTGTTTGGTGTCCCGCAGCTGAGCCAC 158
 QY 121 AAGAGTTCTGAAGATTCGGTGCATATCTGTCCACCTTATGAAACATCATGTGG 180
 DB 159 AAGAGTTCTGAAGATTCGGTGCATATCTGTCCACCTTATGAAACATCATGTGG 218

QY 181 CATATTTACACACAGAAATGTATCCACAGAGGACTGCNACTGCCTGCACGTGGTGAGCCC 240
 DB 219 CACATTTACACACAGAAATGTATCCACAGAGGACTGCNACTGCCTGCACGTGGTGAGCCC 278
 QY 241 ATGCCAGTGCCTGGCCATGACCTGGAGGCTTACTGCCTGCTGTGGAGTGCAGGTACGAG 300
 DB 279 ATGCCAGTGCCTGGCCATGACCTGGAGGCTTACTGCCTGCTGTGGAGTGCAGGTACGAG 338
 QY 301 GAGGCGACACACACACATCAAGGTCAATCATTTGTCATCTACCTGTCCGTGGTGGTGGC 360
 DB 339 GAGGCGACACACACACATCAAGGTCAATCATTTGTCATCTACCTGTCCGTGGTGGTGGC 398
 QY 361 CTGTTGCTCTACATGGCTTCTGTGATGCTGGTGGACCTCTGATCCGAAGCCGGATGCA 420
 DB 399 CTGTTGCTCTACATGGCTTCTGTGATGCTGGTGGACCTCTGATCCGAAGCCGGATGCA 458
 QY 421 TACACTGACCAACTGCACATGAGGAGGAGATGAGGATGCTCGCTCTATGGCAGAGCT 480
 DB 459 TAYACTGACCAACTGCACATGAGGAGGAGATGAGGATGCTCGCTCTATGGCAGAGCT 518
 QY 481 GCTGATTCCTCGGGGGACCCCGAGAAAACACAGTCTGTGGAGGCTGTGAAAGTGGCAG 540
 DB 519 GCTGATTCCTCGGGGGACCCCGAGAAAACACAGTCTGTGGAGGCTGTGAAAGTGGCAG 578
 QY 541 CAGGCTGTGAAGCTGCAGGTGCAGGAGCAGGAGACAGTCTTCGATCCGACACAGATG 600
 DB 579 CAGGCTGTGAAGCTGCAGGTGCAGGAGCAGGAGACAGTCTTCGATCCGACACAGATG 638
 QY 601 CTCAGCTAGATGGGCTGGTGTGGTCAAGGCCACCAACACATGGCTGCCAGTCTCC 660
 DB 639 CTCAGCTAGATGGGCTGGTGTGGTCAAGGCCACCAACACATGGCTGCCAGTCTCC 698
 QY 661 AGGCTGCACAAAGCAGGGGGTACTTCTCCCTCCCTCGGTTCACATCTTCCCTTAAAA 720
 DB 699 AGGCTGCACAAAGCAGGGGGTACTTCTCCCTCCCTCGGTTCACATCTTCCCTTAAAA 758
 QY 721 GCTGTGGCATTTTCTCCCTTCTCCCTAACCTTAGAATGTGTACTTGGCTATTTGA 780
 DB 759 GCTGTGGCATTTTCTCCCTTCTCCCTAACCTTAGAATGTGTACTTGGCTATTTGA 818
 QY 781 TTAGGAAGAGGAGTGTGGTCTCTGATCTGTGTGTCTTGGGTCTTTGGGGTTGAG 840
 DB 819 TTAGGAAGAGGAGTGTGGTCTCTGATCTGTGTGTCTTGGGTCTTTGGGGTTGAG 878
 QY 841 GATGGGAAGCAGGCCACAGAGGGAATGGAGACATTCAGGGGGCTCAGGAGTGGATG 900
 DB 879 GATGGGAAGCAGGCCACAGAGGGAATGGAGACATTCAGGGGGCTCAGGAGTGGATG 938
 QY 901 CGATCTGTCTCTCTGGCTCCACTCTTGCCGCTTCCAGCTCTGAGTCTTGGGAATGTG 960
 DB 939 CGATCTGTCTCTCTGGCTCCACTCTTGCCGCTTCCAGCTCTGAGTCTTGGGAATGTG 998
 QY 961 TTACCTTGGAGATAAAGCTGGGTCTTCAGGAACCTCAGTGTGGGAGGAAGCATGGC 1020
 DB 999 TTACCTTGGAGATAAAGCTGGGTCTTCAGGAACCTCAGTGTGGGAGGAAGCATGGC 1058
 QY 1021 CCAGCATCAGCATGTGTCTTCTGTGAGTGGTTC-TTATCACCACCTCCCTCCAGAC 1079
 DB 1059 CCAGCATCAGCATGTGTCTTCTGTGAGTGGTCTTATCACCACCTCCCTCCAGAC 1118
 QY 1080 CCAGCGCTCAGCGCCACCGCCAGCTCCAGCGCTCAGGACAGCTCTGATGGGAGAGCTGG 1139
 DB 1119 CCAGCGCTCAGCGCCACCGCCAGCTCCAGCGCTCAGGACAGCTCTGATGGGAGAGCTGG 1178

RESULT 6	
ABQ91986	
ID	ASQ91956 standard; cDNA; 1562 BP.
XX	
AC	ABQ91986;
XX	
DI	30-SEP-2002 (first entry)
XX	
DE	Human NF-kB activating gene SEQ ID NO 150.
XX	
KW	Human; NF-kB; nuclear factor kappa B; mouse; antiinflammatory;
KW	immunomodulator; cytostatic; antineoplastic; osteopathic; neoplastic;
KW	neuroprotective; anti-HIV; autoimmune disease; cancer; infection;
KW	bone disease; AIDS; neurodegenerative disease; ischaemic disorder; gene;
KW	ss.
XX	
OS	Homo sapiens.
XX	
PN	W0200253737-A1.
XX	
PD	11-JUL-2002.
XX	
PF	25-DEC-2001; 2001WO-JP011389.
XX	
PR	28-DEC-2000; 2000JP-00402288.
PR	26-MAR-2001; 2001JP-00088912.
PR	24-AUG-2001; 2001JP-00254018.
XX	
PA	(ASAH) ASAH KASEI KOGYO KK.
XX	
PI	Matsuda A, Honda G, Muramatsu S, Nagano Y;
XX	
DR	WPI; 2002-583617/62.
DR	P-PSDB; ABP61498.
XX	
PT	NF-approximatelykB activating gene and expressed protein, applicable in
PT	diagnosis and screening inhibitors or promoters to control excessive

123	AAAGCTTTATCTTTGGTGGCTGTGGTCGGGTGTTTGGTGGTGGCCCAAGCTGAAGCAAC	182
124		
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AC	AA399393;
XX	
XX	16-OCT-2000 (first entry)
XX	
XX	Human TANGO 183 cDNA.
XX	
XX	TANGO 180; TANGO 181; TANGO 182; TANGO 183; TANGO 184; TANGO 185;
XX	TANGO 186; TANGO 188; TANGO 189; TANGO 215; TANGO 187; human; murine;
XX	secreted protein; transmembrane protein; gene therapy; vaccine;
XX	diagnosis; treatment; detection; ss.
XX	
XX	Hom sapiens.
XX	
XX	Key Location/Qualifiers
XX	CDS 96..647
XX	FT /*tag= a
XX	FT /*product= "TANGO 183"
XX	
XX	W0200018904-A2.
XX	
XX	06-APR-2000.
XX	
XX	30-SEP-1999; 99WO-US022817.
XX	
XX	30-SEP-1998; 98US-00164220.
XX	
XX	02-OCT-1998; 98US-00164169.
XX	
XX	(MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX	
XX	Barnes TM;
XX	
XX	WPI; 2000-293144/25.
XX	
XX	P-PSDB; AAY88274.
XX	
XX	Isolated nucleic acids encoding TANGO polypeptides useful for preventing,
XX	diagnosing and treating diseases associated with inappropriate protein
XX	expression.
XX	
XX	Claim 1c; Fig 7; 249pp; English.
XX	
XX	This invention describes novel human and murine nucleic acids encoding
XX	TANGO polypeptides (which are either wholly secreted or transmembrane
XX	proteins) which can be used for gene therapy and/or vaccination. The
XX	peptides are designated TANGO 180 to TANGO 189 and TANGO 215. The nucleic
XX	acids may be used to produce TANGO 180 to TANGO 189 and TANGO 215
XX	polypeptides according to standard recombinant DNA methodologies. They
XX	may also be used to detect and quantify the presence of TANGO nucleic
XX	acids in a sample and therefore identify or diagnose diseases associated
XX	with inappropriate TANGO expression (e.g. diseases related to over or
XX	under expression of the polypeptides or the expression of inactive
XX	polypeptides). The nucleic acids and the polypeptides they encode may be
XX	used according to standard gene therapy protocols, to treat diseases
XX	associated with inappropriate TANGO expression by supplementing a
XX	patients own production of the polypeptide of to rectify mutations that
XX	may result in expression of an abnormally active polypeptide. The
XX	polypeptides may also be used to identify and produce agonists and
XX	antagonists of TANGO expression and activity which may be used to
XX	modulate TANGO related processes and diseases. The polypeptides are
XX	particularly useful for use as antigens for producing antibodies to TANGO
XX	proteins which may be used for inhibiting the activity of TANGO proteins.
XX	They may also be used to detect and quantify the presence of TANGO
XX	proteins in samples and therefore identify patients in whom the protein
XX	is over- or under-expressed. This sequence encodes the human TANGO 183

CC proteins which may be used for inhibiting the activity of TANGO proteins.
CC particularly useful for use as antigens for producing antibodies to TANGO
CC proteins.
CC They may also be used to detect and quantify the presence of TANGO
CC proteins in samples and therefore identify patients in whom the protein
CC is over- or under-expressed. This sequence encodes the human TANGO 183

XX 18-AUG-2000; 2000WO-IB001496.
 PF 18-AUG-1999; 99US-0149499p.
 PR 28-SEP-1999; 99US-0156503p.
 XX (GEHU-) GERMAN HUMAN GENOME PROJECT.
 PA Wiemann S;
 PI WPI; 2001-327840/34.
 DR P-PSDB; AB052631.
 XX Nucleic acids having the sequences of clones isolated from libraries of
 PT different human tissues, useful in recombinant DNA methodologies.
 XX Claim 1; Page 144; 1095pp; English.
 CC This invention describes novel polynucleotides and polypeptides isolated
 CC from human cDNA libraries which can be used for gene therapy or in
 CC vaccines. The polynucleotides of the invention and antibodies encoded by
 CC them may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate polypeptide expression. The products of the
 CC invention may also be used to identify modulators of expression and
 CC activity and to down regulate expression and activity. The antibodies of
 CC the invention may also be used as diagnostic agents for detecting the
 CC presence of polypeptides in samples. This sequence encodes a polypeptide
 CC described in the disclosure of the invention
 XX
 SQ Sequence 1552 BP; 318 A; 412 C; 444 G; 378 T; 0 U; 0 Other;

Query Match 98.4%; Score 1475; DB 5; Length 1552;

Best local Similarity 99.3%; Pred. No. 0;
 Matches 1494; Conservative 0; Mismatches 5; Indels 6; Gaps 1;

QY 1 GGGGCTGACAGGGGCTTTAGGTGTGGGCTTTGCTGACCAAGAGCTGATAAGCATG 60
 DB |||||
 QY 61 AAGCTCTTATCTTTGGTGGCGGTGGTGGGTTTGGTGGTGGTGGTGGTGGTGGTGG 120
 DB |||||
 QY 84 AAGCTCTTATCTTTGGTGGCTGGTGGGTTTGGTGGTGGTGGTGGTGGTGGTGG 143
 QY 121 AAGAGTTCTGAAGATTCGGTGCATATGCAATGCAATGCAATGCAATGCAATGCAATG 180
 DB 144 AAGAGTTCTGAAGATTCGGTGCATATGCAATGCAATGCAATGCAATGCAATGCAATG 203
 QY 181 CATATTACACCAAGATGTATCCAGAGAGACT-----GCAACTGCCTGCAGTGGTG 234
 DB 204 CACATTTACACCAAGATGTATCCAGAGAGACTGTGTAGCAACTGCCTGCAGTGGTG 263
 QY 235 GAGCCATGCAATGCTGCTGGGCTGAGGTGGAGGCTGCTGCTGCTGCTGCTGCTGCTG 294
 DB 264 GAGCCATGCAATGCTGCTGGGCTGAGGTGGAGGCTGCTGCTGCTGCTGCTGCTGCTG 323
 QY 295 TAGGAGGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 354
 DB 324 TAGGAGGCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 383
 QY 355 GGTGGCCTGTTGCTCTACATGGCCTTCCCTGATGCTGGTGGAGCCCTCTGATCCGAAAGCG 414
 DB 384 GGTGGCCTGTTGCTCTACATGGCCTTCCCTGATGCTGGTGGAGCCCTCTGATCCGAAAGCG 443

QY 415 GATGCATACACTGACAACTGCACAAATGAGAGAGAGATGAGGATGCTGGCTCTATGGCA 474
 DB |||||
 QY 444 GATGCATACACTGACAACTGCACAAATGAGAGAGAGATGAGGATGCTGGCTCTATGGCA 503
 DB |||||
 QY 475 GCAGCTGCTGCATCCCTGGGGGAGCCCGAGCAAAACACAGTCCCTGGAGCGTGTGGAGGT 534
 DB |||||
 QY 504 GCAGCTGCTGCATCCCTGGGGGAGCCCGAGCAAAACACAGTCCCTGGAGCGTGTGGAGGT 563
 DB |||||
 QY 535 GCGCAGCAGCGGTGGAAGTGCAGGTGCAGAGCAGCGGAAAGACAGTCTTTCGATCGGCAC 594
 DB |||||
 QY 564 GCGCAGCAGCGGTGGAAGTGCAGGTGCAGAGCAGCGGAAAGACAGTCTTTCGATCGGCAC 623
 DB |||||
 QY 595 AAGATGCTCAGCTAGATGGGCTGGTGTGGTGGGTCAGAGCCGCCAACACACATGGCTGCCA 654
 DB |||||
 QY 624 AAGATGCTCAGCTAGATGGGCTGGTGTGGTGGGTCAGAGCCGCCAACACACATGGCTGCCA 683
 DB |||||
 QY 655 GCTTCCAGGCTGCACAAAGCAGGGGCTACTCTCCCTGGCTGGTGGTGGTGGTGGTGGTGG 714
 DB |||||
 QY 684 GCTTCCAGGCTGCACAAAGCAGGGGCTACTCTCCCTGGCTGGTGGTGGTGGTGGTGGTGG 743
 DB |||||
 QY 715 TTAAAGCTGTGGGATTTTCTCCTTCGCCCTTACTTTAGAAATGTTGACTTGGCTA 774
 DB |||||
 QY 744 TTAAAGCTGTGGGATTTTCTCCTTCGCCCTTACTTTAGAAATGTTGACTTGGCTA 803
 DB |||||
 QY 775 TTTGATTAGGGAAGAGGGATGCTGATCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 834
 DB |||||
 QY 804 TTTGATTAGGGAAGAGGGATGCTGATCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 863
 DB |||||
 QY 835 TTGAAGGAGTGGGGAAGCAGGCGCAGAGGGAATGAGACATTCAGAGGCGCTCAGAG 894
 DB |||||
 QY 864 TTGAAGGAGGGAAGCAGGCGCAGAGGGAATGAGACATTCAGAGGCGCTCAGAG 923
 DB |||||
 QY 895 TGGATGAGTCTGTCTCTCTGGCTCCACTCTTGGCGGCTTCAGAGCTCTGAGTCTTGGGA 954
 DB |||||
 QY 924 TGGATGAGTCTGTCTCTCTGGCTCCACTCTTGGCGGCTTCAGAGCTCTGAGTCTTGGGA 983
 DB |||||
 QY 955 ATGTTGTATCCCTTGAAGATTAAGCTGGTCTTCAGAGACTCAGTCTCTGAGGGAAG 1014
 DB |||||
 QY 984 ATGTTGTATCCCTTGAAGATTAAGCTGGTCTTCAGAGACTCAGTCTCTGAGGGAAG 1043
 DB |||||
 QY 1015 CATGGCCACCAATTCAGCATGTGTTCCTTTCTGAGTGGTGTCTTATCAACAACCTCCCTCC 1074
 DB |||||
 QY 1044 CATGGCCACCAATTCAGCATGTGTTCCTTTCTGAGTGGTGTCTTATCAACAACCTCCCTCC 1103
 DB |||||
 QY 1075 CAGCCACAGGCTCAGCCCAAGCCAGCTCCAGGCTCAGGACAGCTCTGATGGGA 1134
 DB |||||
 QY 1104 CAGCCACAGGCTCAGCCCAAGCCAGCTCCAGGCTCAGGACAGCTCTGATGGGA 1163
 DB |||||
 QY 1135 GCTGGGCCCCCTGAGCCCACTGGGTCTTCAGGCTGCAGTGGAAAGCTGGTGGTGGTGGTGG 1194
 DB |||||
 QY 1164 GCTGGGCCCCCTGAGCCCACTGGGTCTTCAGGCTGCAGTGGAAAGCTGGTGGTGGTGGTGG 1223
 DB |||||
 QY 1195 CTTGTGCACTCTCGGACTGGGCGATGGAGTGGCGATGCACTCTCTGGCGGCTCCCT 1254
 DB |||||
 QY 1224 CTTGTGCACTCTCGGACTGGGCGATGGAGTGGCGATGCACTCTCTGGCGGCTCCCT 1283
 DB |||||
 QY 1255 CACTGCACTCTGAGGCTGGGCGATGGAGTGGCGATGCACTCTCTGGCGGCTCCCT 1314
 DB |||||
 QY 1284 CACTGCACTCTGAGGCTGGGCGATGGAGTGGCGATGCACTCTCTGGCGGCTCCCT 1343
 DB |||||
 QY 1315 CAGCGGTGGTGGAAATGAGCTCAGAGGCTGAGGCTGGATCTGAAACCAACCAAGCG 1374
 DB |||||
 QY 1344 CAGCGGTGGTGGAAATGAGCTCAGAGGCTGAGGCTGGATCTGAAACCAACCAAGCG 1403
 DB |||||

QY	1375	TGTACTGGGTTCCCTCTTCTTCTGTCCTGAACTTCGTTGTACCAAGTCCATGGAGAGAAATTT	1434	PR	17-SEP-1998;	98US-0100684P.
				PR	17-SEP-1998;	98US-0100710P.
Db	1404	TGTACTGGGTTCCCTCTTCTTCTGTCCTGAACTTCGTTGTACCAAGTCCATGGAGAGAAATTT	1463	PR	17-SEP-1998;	98US-0100919P.
				PR	17-SEP-1998;	98US-0100930P.
QY	1435	TGTCTCTTCTGTAGTTGTCTGTAAATCAAGAGCCATCATTAATAATGTTTATT	1494	PR	18-SEP-1998;	98US-0100848P.
				PR	18-SEP-1998;	98US-0100849P.
Db	1464	TGTCTCTTCTGTAGTTGTCTGTAAATCAAGAGCCATCATTAATAATGTTTATT	1523	PR	18-SEP-1998;	98US-0101014P.
				PR	18-SEP-1998;	98US-0101068P.
QY	1495	CTCTC 1499		PR	18-SEP-1998;	98US-0101071P.
				PR	22-SEP-1998;	98US-0101279P.
Db	1524	CTCTC 1528		PR	23-SEP-1998;	98US-0101471P.
				PR	23-SEP-1998;	98US-0101472P.
				PR	23-SEP-1998;	98US-0101473P.
				PR	23-SEP-1998;	98US-0101476P.
				PR	23-SEP-1998;	98US-0101477P.
				PR	23-SEP-1998;	98US-0101479P.
				PR	24-SEP-1998;	98US-0101736P.
				PR	24-SEP-1998;	98US-0101741P.
				PR	24-SEP-1998;	98US-0101743P.
				PR	24-SEP-1998;	98US-0101913P.
				PR	24-SEP-1998;	98US-0101916P.
				PR	29-SEP-1998;	98US-0102207P.
				PR	29-SEP-1998;	98US-0102240P.
				PR	29-SEP-1998;	98US-0102307P.
				PR	29-SEP-1998;	98US-0102330P.
				PR	29-SEP-1998;	98US-0102331P.
				PR	30-SEP-1998;	98US-0102484P.
				PR	30-SEP-1998;	98US-0102487P.
				PR	30-SEP-1998;	98US-0102570P.
				PR	30-SEP-1998;	98US-0102571P.
				PR	01-OCT-1998;	98US-0102684P.
				PR	01-OCT-1998;	98US-0102687P.
				PR	02-OCT-1998;	98US-0102965P.
				PR	06-OCT-1998;	98US-0103258P.
				PR	06-OCT-1998;	98US-0103443P.
				PR	07-OCT-1998;	98US-0103314P.
				PR	07-OCT-1998;	98US-0103315P.
				PR	07-OCT-1998;	98US-0103328P.
				PR	07-OCT-1998;	98US-0103393P.
				PR	07-OCT-1998;	98US-0103396P.
				PR	07-OCT-1998;	98US-0103401P.
				PR	08-OCT-1998;	98US-0103633P.
				PR	08-OCT-1998;	98US-0103678P.
				PR	08-OCT-1998;	98US-0103679P.
				PR	08-OCT-1998;	98US-0103711P.
				PR	14-OCT-1998;	98US-0104257P.
				PR	20-OCT-1998;	98US-0104987P.
				PR	20-OCT-1998;	98US-0105000P.
				PR	21-OCT-1998;	98US-0105002P.
				PR	21-OCT-1998;	98US-0105104P.
				PR	22-OCT-1998;	98US-0105169P.
				PR	22-OCT-1998;	98US-0105266P.
				PR	26-OCT-1998;	98US-0105693P.
				PR	26-OCT-1998;	98US-0105694P.
				PR	27-OCT-1998;	98US-0105607P.
				PR	27-OCT-1998;	98US-0105861P.
				PR	27-OCT-1998;	98US-0105862P.
				PR	27-OCT-1998;	98US-0106062P.
				PR	28-OCT-1998;	98US-0106023P.
				PR	28-OCT-1998;	98US-0106029P.
				PR	28-OCT-1998;	98US-0106030P.

AAA37041
 ID AAA37041 standard; cDNA; 1564 BP.
 XX
 AC AAA37041;
 XX
 DT 08-AUG-2000 (first entry)
 XX
 DE Human PRO1248 (UNQ631) cDNA sequence SEQ ID NO:67.
 XX
 KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
 KW transmembrane; secretion; immunoadhesion; pharmaceutical; screening; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200012706-A2.
 XX
 PD 09-MAR-2000.
 XX
 PF 01-SEP-1999; 99WO-JS020111.
 XX
 PR 01-SEP-1998; 98US-0098716P.
 PR 01-SEP-1998; 98US-0098749P.
 PR 01-SEP-1998; 98US-0098750P.
 PR 02-SEP-1998; 98US-0098803P.
 PR 02-SEP-1998; 98US-0098821P.
 PR 02-SEP-1998; 98US-0098843P.
 PR 09-SEP-1998; 98US-0099536P.
 PR 09-SEP-1998; 98US-0099596P.
 PR 09-SEP-1998; 98US-0099598P.
 PR 09-SEP-1998; 98US-0099602P.
 PR 09-SEP-1998; 98US-0099642P.
 PR 10-SEP-1998; 98US-0099741P.
 PR 10-SEP-1998; 98US-0099754P.
 PR 10-SEP-1998; 98US-0099763P.
 PR 10-SEP-1998; 98US-0099792P.
 PR 10-SEP-1998; 98US-0099808P.
 PR 10-SEP-1998; 98US-0099812P.
 PR 10-SEP-1998; 98US-0099813P.
 PR 10-SEP-1998; 98US-0099816P.
 PR 15-SEP-1998; 98US-0100389P.
 PR 15-SEP-1998; 98US-0100390P.
 PR 16-SEP-1998; 98US-0100584P.
 PR 16-SEP-1998; 98US-0100627P.
 PR 16-SEP-1998; 98US-0100661P.
 PR 16-SEP-1998; 98US-0100662P.
 PR 16-SEP-1998; 98US-0100664P.
 PR 17-SEP-1998; 98US-0100663P.

28-OCT-1998; 98US-0106032P.
28-OCT-1998; 98US-0106033P.
28-OCT-1998; 98US-0106178P.
29-OCT-1998; 98US-0106248P.
29-OCT-1998; 98US-0106384P.
29-OCT-1998; 98US-0108500P.
30-OCT-1998; 98US-0106464P.
03-NOV-1998; 98US-0106856P.
03-NOV-1998; 98US-0106902P.
03-NOV-1998; 98US-0106919P.
03-NOV-1998; 98US-0106932P.
03-NOV-1998; 98US-0106934P.
10-NOV-1998; 98US-0107783P.
17-NOV-1998; 98US-0108773P.
17-NOV-1998; 98US-0108779P.
17-NOV-1998; 98US-0108787P.
17-NOV-1998; 98US-0108788P.
17-NOV-1998; 98US-0108801P.
17-NOV-1998; 98US-0108802P.
17-NOV-1998; 98US-0108806P.
17-NOV-1998; 98US-0108807P.
17-NOV-1998; 98US-0108867P.
18-NOV-1998; 98US-0108848P.
18-NOV-1998; 98US-0108849P.
18-NOV-1998; 98US-0108850P.
18-NOV-1998; 98US-0108851P.
18-NOV-1998; 98US-0108852P.
18-NOV-1998; 98US-0108858P.
18-NOV-1998; 98US-0108904P.
(GETH) GENENTECH INC.
Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;
WPI; 2000-237871/20.
P-PSDs; AA99359.
New mammalian DNA sequences encoding transmembrane, receptor or secreted
PRO polypeptides, useful for screening of potential peptide or small
molecule inhibitors of the relevant receptor/ligand interactions.
Claim 2; Fig 39; 773pp; English.
AAA37022 to AAA37144 encode the new isolated human transmembrane,
receptor or secreted PRO polypeptides given in AA99340 to AA993462. The
transmembrane and receptor PRO proteins can be used for screening of
potential peptide or small molecule inhibitors of the relevant
receptor/ligand interactions. The polypeptides and nucleotide sequences
encoding then have various industrial applications, including uses as
pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR
primers and hybridisation probes used in the isolation of the PRO
polypeptides from the present invention.
Sequence 1564 BP; 314 A; 430 G; 441 G; 379 T; 0 U; 0 Other;
Query Match 98.3%; Score 1473.6; DB 3; Length 1564;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1476; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
20 AGGTGTGGGCTTGTGCTGGCCGACAGGCTGATTAAGCATGAGCTCTATCTTTGGTGG 79
|||||

84 AGGTGTGGGCTTGTGCTGGCCGACAGGCTGATTAAGCATGAGCTCTATCTTTGGTGG 143
QY
80 CCGTGGTGGGCTTGTGCTGGTGGCCGCCAGCTGAAGCCAAACAGAGTCTGAAGATATCC 139
D
144 CTGTGGTGGGCTTGTGCTGGTGGCCGCCAGCTGAAGCCAAACAGAGTCTGAAGATATCC 203
QY
140 GGTGCANATGATCTGTGCACCTTATAGAAACATCAGTGGGCAATATTTACAAACAGAAAG 199
D
204 GGTGCANATGATCTGTGCACCTTATAGAAACATCAGTGGGCAATATTTACAAACAGAAAG 263
QY
200 TATCCGAGAAGGACTGCANACTGCTGCACGCTGGTGGAGCCCATGCCAGTGGCTGGCCATG 259
D
264 TATCCGAGAAGGACTGCANACTGCTGCACGCTGGTGGAGCCCATGCCAGTGGCTGGCCATG 323
QY
260 AGGTGGAGGCTACTGCTGCTGTGCGAGTGCAGGTAAAGAGAGAGAGAGAGAGAGAGAGAG 319
D
324 AGGTGGAGGCTACTGCTGCTGTGCGAGTGCAGGTAAAGAGAGAGAGAGAGAGAGAGAGAG 383
QY
320 TCAAGGTGATCATCTGATCATCTGCTGCTGCTGGTGGGCTGGCTGGCTGGCTGGCTGGCT 379
D
384 TCAAGGTGATCATCTGATCATCTGCTGCTGCTGGTGGGCTGGCTGGCTGGCTGGCTGGCT 443
QY
380 TCTGTGCTGGTGGAGCCCTCTGATCCGAAAGCGGAGTGCATACACTGAGCAACTGCACA 439
D
444 TCTGTGCTGGTGGAGCCCTCTGATCCGAAAGCGGAGTGCATACACTGAGCAACTGCACA 503
QY
440 ATGAGAGAGAGATGAGGATGCTGCTGTATGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 499
D
504 ATGAGAGAGAGATGAGGATGCTGCTGTATGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 563
QY
500 CCGAGGCAAAACAGTCTGAGGCTGTGGAAGTGCCTGAGGCTGCCAGAGAGAGAGAGAGAGAG 559
D
564 CCGAGGCAAAACAGTCTGAGGCTGTGGAAGTGCCTGAGGCTGCCAGAGAGAGAGAGAGAGAG 623
QY
560 TGCAGAGAGAGAGAGAGAGAGTCTTGCATCGGCAACAGATGCTCAGCTAGATGGGCTGGT 619
D
624 TGCAGAGAGAGAGAGAGAGTCTTGCATCGGCAACAGATGCTCAGCTAGATGGGCTGGT 683
QY
620 GTGGTGGGCTCAAGGCGCCCAACACCATGGCTGCCAGCTTCCAGGCTGGAGAGAGAGAGAG 679
D
684 GTGGTGGGCTCAAGGCGCCCAACACCATGGCTGCCAGCTTCCAGGCTGGAGAGAGAGAGAG 743
QY
680 GCTACTTCTCCCTCCCTCGGTTCCAGTCTTCCCTTTAAAGGCTGTGGCATTTTCTCTC 739
D
744 GCTACTTCTCCCTCCCTCGGTTCCAGTCTTCCCTTTAAAGGCTGTGGCATTTTCTCTC 803
QY
740 CTTCTCCCTAACTTTAGAAATGTTGACTTGGCTATTTTATTAGGAGAGAGAGATGGTGG 799
D
804 CTTCTCCCTAACTTTAGAAATGTTGACTTGGCTATTTTATTAGGAGAGAGAGATGGTGG 863
QY
800 TCTCTGATCTCTGTTCTCTCTTGGGCTCTTTGGGCTTGAAGGATGGGAGAGAGAGAGAGAG 859
D
864 TCTCTGATCTCTGTTCTCTCTTGGGCTCTTTGGGCTTGAAGGAGAGAGAGAGAGAGAGAG 923
QY
860 GAAGGAGATGAGACATTCGAGGCGGCTTCAGAGTGGATGATGCTGCTCTCTCTGCTCT 919
D
924 GAAGGAGATGAGACATTCGAGGCGGCTTCAGAGTGGATGATGCTGCTCTCTCTGCTCT 983
QY
920 CCACTCTTGGCGGCTTCCAGCTCTGAGTCTTGGGATGTTGTTACCTTGGAGAGAGAGAGAG 979
D
984 CCACTCTTGGCGGCTTCCAGCTCTGAGTCTTGGGATGTTGTTACCTTGGAGAGAGAGAGAG 1043
QY
980 CTGGGCTCTTCAGGAGACTCAGTGTCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1039

16-DEC-1999; 99WO-US0030095.
 PR
 03-JAN-2000; 2000WO-US000219.
 PR
 06-JAN-2000; 2000WO-US000376.
 PR
 (GETH) GENENTECH INC.
 PPA
 PPA
 Baker KP, Botstein D, Desnovers Z, Eaton DL, Ferrara N, Fong S;
 PPI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
 PPI Pan J, Paoni NF, Roy NA, Smith V, Stewart TA, Tumas D, Watanabe CK;
 PPI Williams PM, Wood WI;
 PPA
 WPI; 2001-071395/08.
 DR
 DR
 XX
 XX
 Secreted and transmembrane proteins and nucleic acids designated PRO,
 PPI useful as hybridization probes, in chromosome and gene mapping and gene
 PPI therapy.
 PT
 PT
 Claim 2; Fig 39; 787pp; English.
 PS
 PS
 PS
 CC The present invention relates to secreted and transmembrane proteins.
 CC These proteins and the DNA encoding them may be used as hybridization
 CC probes, in chromosome and gene mapping and in the generation of anti-
 CC sense RNA and DNA. They may also be used to generate either
 CC transgenic animals or knockout animals which are in turn useful for
 CC development and screening of therapeutically useful reagents. The nucleic
 CC acids may also be used in gene therapy
 XX
 XX
 Sequence 1564 BP; 314 A; 430 C; 441 G; 379 T; 0 U; 0 Other;
 SQ
 Query Match 98.3%; Score 1473.6; DB 4; Length 1564;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1476; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 20 AGGTGTCCGGTCTTGCTGGCCAGCAAGCGCTGATAGCATGAAGCTCTTACTTGTGGG 79

Qy 80 CCGTGGTCGGGTGTTTGTGCTGGTGCCTGAGCCCAACAAGAGTTCGAGATATCC 139

[illegible]

Db 144 CTGTGGTCGGGTGTTTGCTGGTGCCCCAGCTGAAGCCACAAGAGTTCTGAAGATATCC 203

22

OV 140 GGTGCAAATGCATCTGTCCACCTTATAGAAACATCAGTGGGCATATTTACAACCAGAATG 199

[illegible]

Db 204 GGTCAAATGCATCTGTCCAOCCTATAGAAACATCAGTGGGCACATTTACACCAAG 263

Qy 200 TATCCCAAGAGGAGTGCACCTGCCTGCACGTGGTGGAGGCCATGCCAGTGCCTGGCCATG 259

D_b 264 TATCCAGAGGACTGCAACTGCCCTGCACGTGGTGGAGCCCATGCCAGTGCCTGGCCATG 323

QY 260 ACGTGGAGGCC"ACTGCCTGCTGTGGAGTGCAGGTACGAGGAGCGCAGCACCA 319

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324 ACGTGGAGGCCTACTGCCTGCTGTGGAGTGCAGGTACGAGGAGCGCAGCAACACCA 383

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320 TCAAGGTCATCATTTGTCACTACCTGTCCGTGGTGGTGCCCTGTTGCTCTACATGGCCT 379

[illegible]

D6 384 TCAAGGTCAATCATTTGTCATCACTGTCCGTGGTGGGTGGCCCTGTTGCTCTACATGGCCT 443

LD 304 TCHASG01CAYICXII191CAYICIAACC191CCGTGG1GGCGTGGCGCTATGAGCT 743

380 TCGTGGACCTCTGATCCGAAAGCCGGATGCAACACTGAGCAACCGACA 439

QY 380 TCCIGATGGTGGACCCICIGATCCGATACCCGATGCATACACIGAGGCACIGCACH 439

14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1

D6 444 TCCGGA: GCTGGTGGACCCCTCTGATCCGAAGCCGGATGCAATACACTGAGCAACTGCACA 503

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Qy 440 ATGAGGAGGAGGATGCTCGCTCTATGGCAGCAGCTGCTGCATCCCTCGGGGAC 499

1. The first step in the process of creating a new product is to identify a market need. This involves conducting market research to understand what consumers want and what gaps exist in the current market. Once a need is identified, the next step is to develop a concept that addresses this need. This often involves brainstorming and prototyping to refine the idea. The third step is to create a business plan, which outlines the financial aspects of the product, including costs, pricing, and revenue projections. This plan is crucial for securing funding and guiding the development process. The fourth step is to develop a prototype, which allows the team to test the product and gather feedback from potential users. Finally, the product is launched into the market, and the team monitors its performance and makes adjustments as needed. Each of these steps is essential for the successful creation and launch of a new product.

PR	02-JUN-2000;	200OWO-US015264.	
PR	05-JUN-2000;	200OOS-0209832P.	
PR	28-JUL-2000;	200OWO-US020710.	
PR	22-AUG-2000;	200OOS-0264848.	
PR	24-AUG-2000;	200OWO-US023328.	
PR	08-NOV-2000;	200OWO-US030952.	
PR	01-DEC-2000;	200OWO-US032678.	
PR	20-DEC-2000;	200OWO-US034956.	
XX			
XX	(GETH)	GENENTECH INC.	
XX			
PI	Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;		
PI	Par J, Smith V, Watanabe CK, Wood WI, Zhang Z;		
XX			
XX	WPI; 2001-602746/68.		
XX	P-PSDB; AAU29146.		
XX			
PT	Novel nucleic acids encoding PRO polypeptides, used to diagnose the		
PT	presence of tumors, such as prostate and breast tumors, in mammals and to		
PT	screen for modulators of the compounds.		
XX			
PS	Claim 2; Fig 245; 774pp; English.		
XX			
CC	Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR		
CC	primers for PRO polypeptides of the invention. The sequences of the		
CC	invention can be used to detect the presence of a tumour in a mammal by		
CC	comparing the level of expression of a PRO polypeptide in a test sample		
CC	of cells from the animal and a control sample of normal cells, whereby a		
CC	higher level of expression in the test sample indicates the presence of a		
CC	tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,		
CC	pigs, goats and rabbits but are preferably human. The polypeptides can be		
CC	used to stimulate tumour necrosis factor (TNF) alpha release from human		
CC	blood, when contacted with it. A specific polypeptide can be used to		
CC	stimulate the proliferation or differentiation of chondrocyte cells. The		
CC	PRO proteins can be used to determine the presence of tumours and also		
CC	susceptibility to tumour development, particularly adrenal, lung, colon,		
CC	breast, prostate, rectal, cervical, or liver tumours, in mammalian		
CC	subjects. The oligonucleotide probes specific for the PRO nucleic acids		
CC	can be used for genetic analysis of individuals with genetic disorders		
XX			
SQ	Sequence 1564 BP; 314 A; 430 G; 441 G; 379 T; 0 U; 0 Other;		
	Query Match 96.3%; Score 1473.6; DB 4; Length 1564;		
	Best Local Similarity 99.7%; Pred. No. 0;		
	Matches 1476; Conservative 0; Mismatches 4; Indels 0; Gaps 0;		
QY	20 AGGTGTCGGGCTTTGCTGGCCCGAAGCGCTGATACAGTGAAGCTCTTATCTTTGGTG 79		
DB	84 AGGTGTCGGGCTTTGCTGGCCCGAAGCGCTGATACAGTGAAGCTCTTATCTTTGGTG 143		
QY	80 CGGTGTCGGGCTTTGCTGGTGGCCCGAAGCGCTGAAGCAACAGAGTTCTGAAGATATCC 139		
DB	144 CTGTGTCGGGCTTTGCTGGTGGCCCGAAGCGCTGAAGCAACAGAGTTCTGAAGATATCC 203		
QY	140 GGTGCAATGCACTGTGCACCTTATAGAACACTCAGTGGGATATTACACACCAAGT 199		
DB	204 GGTGCAATGCACTGTGCACCTTATAGAACACTCAGTGGGATATTACACACCAAGT 263		
QY	200 TATCCACAGAGGACTGCAACTGCTTCAGCTGGTGGAGGCCCATGCCAGTGCCTGGCAGT 259		
DB	264 TATCCACAGAGGACTGCAACTGCTTCAGCTGGTGGAGGCCCATGCCAGTGCCTGGCAGT 323		
QY	260 ACGTGGAGGCGCTACTGCTGCTGTGGAGTGCAGGTACGAGAGCGGAGCAGCACCAACCA 319		

Db	324	ACGTGGAAGGCTACTAGCTGCTGCGAGGTGCAGGTGATGAGAGGCGCAGACCAACCA	383
Qy	320	TCAAAGTCATCATTTGTCATCTACCTGTCCTGTCGTCGGTGGCCTGTTGCTCTACATGGCCT	379
Db	384	TCAAAGTCATCATTTGTCATCTACCTGTCCTGTCGTCGGTGGCCTGTTGCTCTACATGGCCT	443
Qy	380	TCTGTATGCTGGTGACGCTCTGATCCGAAGCCGGATGATACACTGAGCAACTGCACA	439
Db	444	TCTGTATGCTGGTGACGCTCTGATCCGAAGCCGGATGATACACTGAGCAACTGCACA	503
Qy	440	ATGAGCAGAGATGAGGATGCTGCTCTATGGCAGCAGTCTGCTGCTCCCTCGGGGAC	499
Db	504	ATGAGCAGAGATGAGGATGCTGCTCTATGGCAGCAGTCTGCTGCTCCCTCGGGGAC	563
Qy	500	CCCGAGCAAAACAATCTGGAGCGTGTGAAAGGTGCGCCAGCAGCGGTGGAAAGCTGCAG	559
Db	564	CCCGAGCAAAACAATCTGGAGCGTGTGAAAGGTGCGCCAGCAGCGGTGGAAAGCTGCAG	623
Qy	560	TGCAGAGCAGCGGAAGACAGTCTGCGATGGCGACAGATGCTCAGATGGGCTGCT	619
Db	624	TGCAGAGCAGCGGAAGACAGTCTGCGATGGCGACAGATGCTCAGATGGGCTGCT	683
Qy	620	GTGGTTGGGTCAAGGCCGCCAACACACATGGCTGCCAGCTTCCAGCTGGCAAAAGCAGGGG	679
Db	684	GTGGTTGGGTCAAGGCCGCCAACACACATGGCTGCCAGCTTCCAGCTGGCAAAAGCAGGGG	743
Qy	680	GCTACTTCTCCCTTCCCTCGGTTCCAGTCTTCCCTTTAAAGCCTGTGGCATTTTCCTC	739
Db	744	GCTACTTCTCCCTTCCCTCGGTTCCAGTCTTCCCTTTAAAGCCTGTGGCATTTTCCTC	803
Qy	740	CTTCTCCCTAACTTAGAAATGTTGTACTTGGCTATTTGATTAGGGAAGGGAATGTGG	799
Db	804	CTTCTCCCTAACTTAGAAATGTTGTACTTGGCTATTTGATTAGGGAAGGGAATGTGG	863
Qy	800	TCTCTGATCTCTGTTCTTCTTGGGTCTTTGGGGTTCAGAGGATGGGGAAGCAGGCCA	859
Db	864	TCTCTGATCTCTGTTCTTCTTGGGTCTTTGGGGTTCAGAGGATGGGGAAGCAGGCCA	923
Qy	860	GAAGGAATGGAACATTCGAGCGGCGCTCAGAGTGGATGGGATGCTCTCTCTGGCT	919
Db	924	GAAGGAATGGAACATTCGAGCGGCGCTCAGAGTGGATGGGATGCTCTCTCTGGCT	983
Qy	920	CCACTCTTGGCGGCTTCCAGCTCTGAGTCTTGGAAATGTTGTTACCTTGGAAAGTAAG	979
Db	984	CCACTCTTGGCGGCTTCCAGCTCTGAGTCTTGGAAATGTTGTTACCTTGGAAAGTAAG	1043
Qy	980	CTGGGCTTCAGAACTCAGTGTCTGGAGAAAGCATGCGCCAGCAATTCAGCATGTGTT	1039
Db	1044	CTGGGCTTCAGAACTCAGTGTCTGGAGAAAGCATGCGCCAGCAATTCAGCATGTGTT	1103
Qy	1040	CTTTCTGCATGTGTTCTTATCACACACTCCCTCCAGGCCGAGGCTCAGGCCCGACCC	1099
Db	1104	CTTTCTGCATGTGTTCTTATCACACACTCCCTCCAGGCCGAGGCTCAGGCCCGACCC	1163
Qy	1100	CCAGCTCCAGGCGCTGAGACAGCTCTGATGGGAGAGCTGGCGCCCTCTGAGCCCATCTGGGT	1159
Db	1164	CCAGCTCCAGGCGCTGAGACAGCTCTGATGGGAGAGCTGGCGCCCTCTGAGCCCATCTGGGT	1223
Qy	1160	CTTCAGGCTGCATGGAGAGTGTGTTGCTGTCCCTGTGCACTCTCGCACTGGGGCA	1219
Db	1224	CTTCAGGCTGCATGGAGAGTGTGTTGCTGTCCCTGTGCACTCTCGCACTGGGGCA	1283

QY	1220	TGAGTGGCCATGCACTACTGCTGGCGTCCCTCACCCTGCACTTGAGGGGTCTGGCA	1279	PR	18-DEC-1997;	97US-0068017P.
DB	1254	TGAGTGGCCATGCACTACTGCTGGCGTCCCTCACCCTGCACTTGAGGGGTCTGGCA	1343	PR	10-MAR-1996;	98US-0077430P.
QY	1280	GTCCCTCTCTCCCACTGCTCCAGTCACTGAGCCAGAGGTGGTTGGAACATGAGAC	1339	PR	11-MAR-1998;	98US-0077649P.
DB	1344	GTCCCTCTCTCCCACTGCTCCAGTCACTGAGCCAGAGGTGGTTGGAACATGAGAC	1403	PR	20-MAR-1998;	98US-0078886P.
QY	1340	TGAGGCTGAGCGTGGATCTGAACACACAGAGCCCTGTACTTGGGTGGCTCTTGTCCCT	1399	PR	20-MAR-1998;	98US-0078939P.
DB	1404	TGAGGCTGAGCGTGGATCTGAACACACAGAGCCCTGTACTTGGGTGGCTCTTGTCCCT	1463	PR	27-MAR-1998;	98US-0079664P.
QY	1400	GAATCTGCTGTACCACTGATGAGAGAGAAATTTCTCTCTTAGAGTTGTGTG	1459	PR	27-MAR-1998;	98US-0079786P.
DB	1464	GAATCTGCTGTACCACTGATGAGAGAGAAATTTCTCTCTTAGAGTTGTGTG	1523	PR	31-MAR-1998;	98US-0080107P.
QY	1460	TAAATCAGGAGGCAATCAATTAATTTTATTTCTCTC	1499	PR	31-MAR-1998;	98US-0080194P.
DB	1524	TAAATCAGGAGGCAATCAATTAATTTTATTTCTCTC	1563	PR	01-APR-1998;	98US-0080327P.
<p>RESULT 12</p> <p>ABX78650</p> <p>ID ABX78650 standard; cDNA; 1564 BP.</p> <p>XX AC ABX78650;</p> <p>XX DT 15-APR-2003 (first entry)</p> <p>XX DE Human PRO polynucleotide #123.</p> <p>XX KW Human; PRO; gene; ss; cytostatic; tumour; cancer; breast; lung; stomach;</p> <p>XX KW liver; dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;</p> <p>XX KW antibody-dependent enzyme mediated produg therapy.</p> <p>XX OS Homo sapiens.</p> <p>XX PN US2003027272-A1.</p> <p>XX PD 06-FEB-2003.</p> <p>XX PF 21-JUN-2002; 2002US-00176492.</p> <p>XX PR 18-SEP-1997; 97US-0059263P.</p> <p>PR 18-SEP-1997; 97US-0059266P.</p> <p>PR 17-OCT-1997; 97US-0062250P.</p> <p>PR 21-OCT-1997; 97US-0063486P.</p> <p>PR 24-OCT-1997; 97US-0063120P.</p> <p>PR 24-OCT-1997; 97US-0063121P.</p> <p>PR 28-OCT-1997; 97US-0063340P.</p> <p>PR 28-OCT-1997; 97US-0063341P.</p> <p>PR 28-OCT-1997; 97US-0063344P.</p> <p>PR 28-OCT-1997; 97US-0063364P.</p> <p>PR 31-OCT-1997; 97US-0063734P.</p> <p>PR 31-OCT-1997; 97US-0063870P.</p> <p>PR 31-OCT-1997; 97US-0064103P.</p> <p>PR 13-NOV-1997; 97US-0065311P.</p> <p>PR 21-NOV-1997; 97US-0066120P.</p> <p>PR 24-NOV-1997; 97US-0066466P.</p> <p>PR 24-NOV-1997; 97US-0066772P.</p> <p>PR 11-DEC-1997; 97US-0069335P.</p> <p>PR 12-DEC-1997; 97US-0069425P.</p> <p>PR 17-DEC-1997; 97US-0069870P.</p>						
PR	18-DEC-1997;	97US-0068017P.				
PR	10-MAR-1996;	98US-0077430P.				
PR	11-MAR-1998;	98US-0077649P.				
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PR	20-MAR-1998;	98US-0078939P.				
PR	27-MAR-1998;	98US-0079664P.				
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PR	31-MAR-1998;	98US-0080107P.				
PR	31-MAR-1998;	98US-0080194P.				
PR	01-APR-1998;	98US-0080327P.				
PR	08-APR-1998;	98US-0081049P.				
PR	08-APR-1998;	98US-0081070P.				
PR	09-APR-1998;	98US-0081195P.				
PR	15-APR-1998;	98US-0081838P.				
PR	21-APR-1998;	98US-0082568P.				
PR	21-APR-1998;	98US-0082569P.				
PR	22-APR-1998;	98US-0082704P.				
PR	22-APR-1998;	98US-0082797P.				
PR	28-APR-1998;	98US-0083322P.				
PR	29-APR-1998;	98US-0083493P.				
PR	29-APR-1998;	98US-0083496P.				
PR	29-APR-1998;	98US-0083499P.				
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PR	05-MAY-1998;	98US-0084366P.				
PR	06-MAY-1998;	98US-0084414P.				
PR	07-MAY-1998;	98US-0084639P.				
PR	07-MAY-1998;	98US-0084643P.				
PR	15-MAY-1998;	98US-0085579P.				
PR	15-MAY-1998;	98US-0085580P.				
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PR	18-MAY-1998;	98US-0086023P.				
PR	22-MAY-1998;	98US-0086392P.				
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PR	28-MAY-1998;	98US-0087208P.				
PR	02-JUN-1998;	98US-0087759P.				
PR	02-JUN-1998;	98US-0087827P.				
PR	03-JUN-1998;	98US-0088025P.				
PR	04-JUN-1998;	98US-0088026P.				
PR	04-JUN-1998;	98US-0088029P.				
PR	04-JUN-1998;	98US-0088033P.				
PR	04-JUN-1998;	98US-0088326P.				
PR	05-JUN-1998;	98US-0088167P.				
PR	05-JUN-1998;	98US-0088202P.				
PR	05-JUN-1998;	98US-0088212P.				
PR	05-JUN-1998;	98US-0088217P.				
PR	09-JUN-1998;	98US-0088653P.				
PR	10-JUN-1998;	98US-0088722P.				
PR	10-JUN-1998;	98US-0088738P.				
PR	10-JUN-1998;	98US-0088740P.				
PR	10-JUN-1998;	98US-0088811P.				
PR	10-JUN-1998;	98US-0088824P.				
PR	10-JUN-1998;	98US-0088823P.				
PR	10-JUN-1998;	98US-0088826P.				
PR	11-JUN-1998;	98US-0088861P.				
PR	11-JUN-1998;	98US-0088863P.				
PR	11-JUN-1998;	98US-0088876P.				
PR	12-JUN-1998;	98US-0089090P.				

PR	12-JUN-1998;	98US-0089105P.	PR	15-SEP-1998;	98US-0100388P.
PR	16-JUN-1998;	98US-0089512P.	PR	16-SEP-1998;	98US-0100662P.
PR	16-JUN-1998;	98US-0089514P.	PR	16-SEP-1998;	98US-0100664P.
PR	17-JUN-1998;	98US-0089538P.	PR	16-SEP-1998;	98US-0101751P.
PR	17-JUN-1998;	98US-0089598P.	PR	16-SEP-1998;	98WO-U501933C.
PR	17-JUN-1998;	98US-0089653P.	PR	17-SEP-1998;	98US-0100683P.
PR	18-JUN-1998;	98US-0089908P.	PR	17-SEP-1998;	98US-0100684P.
PR	19-JUN-1998;	98US-0089952P.	PR	17-SEP-1998;	98US-0100919P.
PR	22-JUN-1998;	98US-0090246P.	PR	17-SEP-1998;	98US-0100932P.
PR	22-JUN-1998;	98US-0090252P.	PR	18-SEP-1998;	98US-0100849P.
PR	22-JUN-1998;	98US-0090254P.	PR	18-SEP-1998;	98US-0101014P.
PR	24-JUN-1998;	98US-0090429P.	PR	18-SEP-1998;	98US-0101068P.
PR	24-JUN-1998;	98US-0090435P.	PR	23-SEP-1998;	98US-0101471P.
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PR	25-JUN-1998;	98US-0090676P.	PR	24-SEP-1998;	98US-0101739P.
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PR	01-JUL-1998;	98US-0091355P.	PR	01-OCT-1998;	98US-0102664P.
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PR	18-AUG-1998;	98US-0097022P.			
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 KW tumour necrosis factor-alpha release; TNF-alpha release;
 KW chondrocyte proliferation; chondrocyte differentiation; tumour;
 KW adrenal tumour; lung tumour; colon tumour; breast tumour;
 KW prostate tumour; rectal tumour; cervical tumour; liver tumour; gene; ss.
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 PD 13-FEB-2003.
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 PF 26-JUN-2002; 2002JS-00183012.
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KW	tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;		
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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

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2	1463.8	99.0	1519	14	US-10-153-668-93	Sequence 93, Appl
3	1481.4	98.8	1645	14	US-10-102-806-218	Sequence 218, App
4	1480	98.7	1562	14	US-10-024-298A-150	Sequence 150, App
5	1480	98.7	1562	14	US-10-042-211A-150	Sequence 150, App

6	1478	98.6	1503	14	US-10-153-668-93	Sequence 93, Appl
7	1473.6	98.3	1564	10	US-09-946-374-67	Sequence 67, Appl
8	1473.6	98.3	1564	12	US-10-206-915-245	Sequence 245, App
9	1473.6	98.3	1564	12	US-10-199-670-245	Sequence 245, App
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23	1473.6	98.3	1564	14	US-10-176-913-245	Sequence 245, App
24	1473.6	98.3	1564	14	US-10-180-552-245	Sequence 245, App
25	1473.6	98.3	1564	14	US-10-180-557-245	Sequence 245, App
26	1473.6	98.3	1564	14	US-10-173-700-245	Sequence 245, App
27	1473.6	98.3	1564	14	US-10-174-572-245	Sequence 245, App
28	1473.6	98.3	1564	14	US-10-174-579-245	Sequence 245, App
29	1473.6	98.3	1564	14	US-10-174-582-245	Sequence 245, App
30	1473.6	98.3	1564	14	US-10-174-588-245	Sequence 245, App
31	1473.6	98.3	1564	14	US-10-175-739-245	Sequence 245, App
32	1473.6	98.3	1564	14	US-10-175-740-245	Sequence 245, App
33	1473.6	98.3	1564	14	US-10-175-743-245	Sequence 245, App
34	1473.6	98.3	1564	14	US-10-176-488-245	Sequence 245, App
35	1473.6	98.3	1564	14	US-10-176-492-245	Sequence 245, App
36	1473.6	98.3	1564	14	US-10-176-747-245	Sequence 245, App
37	1473.6	98.3	1564	14	US-10-176-750-245	Sequence 245, App
38	1473.6	98.3	1564	14	US-10-176-987-245	Sequence 245, App
39	1473.6	98.3	1564	14	US-10-176-992-245	Sequence 245, App
40	1473.6	98.3	1564	14	US-10-176-993-245	Sequence 245, App
41	1473.6	98.3	1564	14	US-10-184-658-245	Sequence 245, App
42	1473.6	98.3	1564	14	US-10-176-991-245	Sequence 245, App
43	1473.6	98.3	1564	14	US-10-173-693-245	Sequence 245, App
44	1473.6	98.3	1564	14	US-10-173-697-245	Sequence 245, App
45	1473.6	98.3	1564	14	US-10-173-697-245	Sequence 245, App

ALIGNMENTS

RESULT 1
US-09-284-320-68
; Sequence 68, Application US/09284320
; Publication No. US20030092175A1
; GENERAL INFORMATION:
; APPLICANT: Kato, Seishi et al.
; TITLE OF INVENTION: HUMAN PROTEINS HAVING TRANSMEMBRANE DOMAINS AND DNAs
; FILE REFERENCE: GIN-6705CFUS
; CURRENT APPLICATION NUMBER: US/09/284,320
; CURRENT FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: JP 8-301429
; PRIOR FILING DATE: 1996-11-13
; PRIOR APPLICATION NUMBER: PCT/JP97/04056
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 68

; LENGTH: 1504

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (63)..(611)
US-09-284-320-68

Query Match 99.7%; Score 1494.2; DB 10; Length 1504;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1496; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGGGCTGAGGGGCTTGTAGTGTCCGGCTTGTGGCCGACGACGCTGATAGCATG 60
Db 6 GGGGCTGAGGGGCTTGTAGTGTCCGGCTTGTGGCCGACGACGCTGATAGCATG 65
QY 61 AAGCTCTTATCTTTGGTGGCGGTGTGGGTGTGGGTGTGGGTGTGGGTGTGGGT 120
Db 66 AAGCTCTTATCTTTGGTGGCGGTGTGGGTGTGGGTGTGGGTGTGGGTGTGGGT 125
QY 121 AAGAGTCTGAAGATTCGGGTGCAATGCATCTGTCCACTTATGAAACATCAATGGG 180
Db 126 AAGAGTCTGAAGATTCGGGTGCAATGCATCTGTCCACTTATGAAACATCAATGGG 185
QY 181 CATATTACACCAAGATGTATCCAGAGGACTGCACTGCTGCAGTGTGGAGCC 240
Db 186 CACATTTACACCAAGATGTATCCAGAGGACTGCACTGCTGCAGTGTGGAGCC 245
QY 241 ATGCCAGTGCCTGGCCATGAGCTGGAGGCTACTGCTGCTGTGGAGTGCAGGTAGAG 300
Db 246 ATGCCAGTGCCTGGCCATGAGCTGGAGGCTACTGCTGCTGTGGAGTGCAGGTAGAG 305
QY 301 GAGCGACGACCCACACATCAAGTTCATCTCATCTACCTGTCCGTGTGGGTGCC 360
Db 306 GAGCGACGACCCACACATCAAGTTCATCTCATCTACCTGTCCGTGTGGGTGCC 365
QY 361 CTGTTGCTTACATGCTCTCCTGATGCTGTGGTGGAGCCCTCTGATCCGAAGCCGATGCA 420
Db 366 CTGTTGCTTACATGCTCTCCTGATGCTGTGGTGGAGCCCTCTGATCCGAAGCCGATGCA 425
QY 421 TACACTGACCAACTGCACAAATGAGAGGAGATGAGGATGCTGCTCTATGGCAGCAGCT 480
Db 426 TACACTGACCAACTGCACAAATGAGAGGAGATGAGGATGCTGCTCTATGGCAGCAGCT 485
QY 481 GCTGCATCCCTCGGGGGACCCGAGCAACACAGTCTCTGAGGCTGTGGAGGTGCCAG 540
Db 486 GCTGCATCCCTCGGGGGACCCGAGCAACACAGTCTCTGAGGCTGTGGAGGTGCCAG 545
QY 541 CAGCGTGGAAAGCTGCAGGTGCGAGGACAGCGAAGACAGTCTTCGATCCGCAACAAGATG 600
Db 546 CAGCGTGGAAAGCTGCAGGTGCGAGGACAGCGGAGACAGTCTTCGATCCGCAACAAGATG 605
QY 601 CTCAGTAGATGGGCTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG 660
Db 606 CTCAGTAGATGGGCTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG 665
QY 661 AGGCTGGACAAACAGGGGGCTACTTCTCCCTCCCTGGTCCAGTCTCCCTTTTAAA 720
Db 666 AGGCTGGACAAACAGGGGGCTACTTCTCCCTCCCTGGTCCAGTCTCCCTTTTAAA 725
QY 721 GCGTGTGGCAATTTTCTCCCTCTCTCCCTAACTTGTAGAAATGTGTACTTGGCTATTGGA 780
Db 726 GCGTGTGGCAATTTTCTCCCTCTCTCCCTAACTTGTAGAAATGTGTACTTGGCTATTGGA 785

QY 781 TTAGGGAAGAGGATGTGGTCTTGATCTCTGTGTGTCTTCTTGGGTCTTGGGTGAG 840
Db 786 TTAGGGAAGAGGATGTGGTCTTGATCTCTGTGTGTCTTCTTGGGTCTTGGGTGAG 845
QY 841 GGATGGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900
Db 846 GGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 905
QY 901 CGATCTGTCTCTCTGGCTCCACTCTTGGCCCTTCCAGCTCTGAGCTTGGGAATGTG 960
Db 906 CGATCTGTCTCTCTGGCTCCACTCTTGGCCCTTCCAGCTCTGAGCTTGGGAATGTG 965
QY 961 TTACCTTGGAGATTAAGCTTGGGTCTTCAAGAACTCAGTGTCTGGAGAAAGCATGGC 1020
Db 966 TTACCTTGGAGATTAAGCTTGGGTCTTCAAGAACTCAGTGTCTGGAGAAAGCATGGC 1025
QY 1021 CCAGCATTCAGCATGTGTCTCTTCTGCAATGTTCTTATCACCACCTCCCTCCAGGCC 1080
Db 1026 CCAGCATTCAGCATGTGTCTCTTCTGCAATGTTCTTATCACCACCTCCCTCCAGGCC 1085
QY 1081 CAGGCGCTCAGGCGCCAGCCGACGCTCCAGCCCTGAGGACAGCTCTGATGGGAGAGCTGG 1140
Db 1086 CAGGCGCTCAGGCGCCAGCCGACGCTCCAGCCCTGAGGACAGCTCTGATGGGAGAGCTGG 1145
QY 1141 CCGCTGAGGCCACTGGGTCTTCAAGGTGCACTGAGAGGCTGTGTGCTGTCCCTGTG 1200
Db 1146 CCGCTGAGGCCACTGGGTCTTCAAGGTGCACTGAGAGGCTGTGTGCTGTCCCTGTG 1205
QY 1201 CACTTCTGCACATGGGGCATGGAGTGCATGATCTCTGCGGTCCCTCCAGCT 1260
Db 1206 CACTTCTGCACATGGGGCATGGAGTGCATGATCTCTGCGGTCCCTCCAGCT 1265
QY 1261 CACTTGAAGGGCTGTGGGCACTGCTCTCTCCCTGCTCCAGCTCTGATGGGAGAGCT 1320
Db 1266 CACTTGAAGGGCTGTGGGCACTGCTCTCTCCCTGCTCCAGCTCTGATGGGAGAGCT 1325
QY 1321 GTGGTGGACATGAGACTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 1380
Db 1326 GTGGTGGACATGAGACTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 1385
QY 1381 TGGGTTGGCTCTGTGCTGAACTTCTGTTGTACAGTGCATGGAGAGAAATTTTGTCT 1440
Db 1386 TGGGTTGGCTCTGTGCTGAACTTCTGTTGTACAGTGCATGGAGAGAAATTTTGTCT 1445
QY 1441 CTGTCTTAGAGTGTGTGTAATCAAGGAAGGCAATCAATAATTTTATTTCTCTC 1499
Db 1446 CTGTCTTAGAGTGTGTGTAATCAAGGAAGGCAATCAATAATTTTATTTCTCTC 1504

RESULT 2

US-10-153-668-95

; Sequence 95, Application US/10153668

; Publication No. US2003092616A1

; GENERAL INFORMATION:

; APPLICANT: HONDA, Goichi

; APPLICANT: MATSUDA, Akio

; APPLICANT: MORIMATSU, Shuji

; APPLICANT: ISHIZAWA, Kenya

; TITLE OF INVENTION: STAT6 Activating Gene

; FILE REFERENCE: 1254-0207P

; CURRENT APPLICATION NUMBER: US/10/153,668

; CURRENT FILING DATE: 2002-05-24

; PRIOR APPLICATION NUMBER: US 60/293,172
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/316,031
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/328,403
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: JP 2001-157043
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: JP 2001-260681
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: JP 2001-313175
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 488
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 95
; LENGTH: 1519
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (79)..(420)
US-10-153-668-95

Query Match 99.0%; Score 1483.8; DB 14; Length 1519;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1496; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 GGGCTGAGCGGCTTTGAGGTGTCGGGCTTTGCTGGCCGACGAGCGCTGATTAAGCATG 60
DB 22 GGGCTGAGCGGCTTTGAGGTGTCGGGCTTTGCTGGCCGACGAGCGCTGATTAAGCATG 81
QY 61 AAGCTCTTATCTTTGCTGGCTGGTGGGTGTTTCTGGTGGCCGACGAGCGCTGATTAAGCATG 120
DB 82 AAGCTCTTATCTTTGCTGGCTGGTGGGTGTTTCTGGTGGCCGACGAGCGCTGATTAAGCATG 141
QY 121 AAGAGTCTGAAGATCCGGTGCAAAATGCAATCTGTCCACCTTATGAACATCAAGTGGG 180
DB 142 AAGAGTCTGAAGATCCGGTGCAAAATGCAATCTGTCCACCTTATGAACATCAAGTGGG 201
QY 181 CATATTACACACAGATGATCCGAGAGGACTGCACTGCTGACGTGGTGGAGGCC 240
DB 202 CATATTACACACAGATGATCCGAGAGGACTGCACTGCTGACGTGGTGGAGGCC 261
QY 241 ATGCCAGTGGCTGGCCATGAGTGGAGGCTACTGCTGCTGGAGTGCAGGTACGAG 300
DB 262 ATGCCAGTGGCTGGCCATGAGTGGAGGCTACTGCTGCTGGAGTGCAGGTACGAG 321
QY 301 GAGCGACGACCAACCAACCAATCAAGGTCAATCTGATCTACCTGTCCGTGGTGGTGGC 360
DB 322 GAGCGACGACCAACCAACCAATCAAGGTCAATCTGATCTACCTGTCCGTGGTGGTGGC 381
QY 361 CTGTTGCTCTACATGGCTTCTGATGCTGGTGGAGCCCTCTGATCCGAAAGCCGGATGCA 420
DB 382 CTGTTGCTCTACATGGCTTCTGATGCTGGTGGAGCCCTCTGATCCGAAAGCCGGATGCA 440
QY 421 TACACTGAGCAACTGCAACATGAGGAGAGATGAGGATGCTGCTCTATGGCAGCACT 480
DB 441 TACACTGAGCAACTGCAACATGAGGAGAGATGAGGATGCTGCTCTATGGCAGCACT 500
QY 481 GGTGCATCCCTCGGGGGACCCCGACCAACACAGTCTGAGAGTGGAGGTGGCCAG 540
DB 501 GGTGCATCCCTCGGGGGACCCCGACCAACACAGTCTGAGAGTGGAGGTGGCCAG 560

QY 541 CAGCGGTGGAAGCTGCAAGTGCAGAGCAGCGGGAAGACAGTCTTCGATCGGCAAGATG 600
DB 561 CAGCGGTGGAAGCTGCAAGTGCAGAGCAGCGGGAAGACAGTCTTCGATCGGCAAGATG 620
QY 601 CTCAGCTAGATGGGCTGCTGTGGTGGGTCAAGGCCCAACACCATGGCTGGCGAGCTCC 660
DB 621 CTCAGCTAGATGGGCTGCTGTGGTGGGTCAAGGCCCAACACCATGGCTGGCGAGCTCC 680
QY 661 AGGCTGGACAAAGCAGGGGGCTACTTCTCCCTTCCCTGGGTCCAGTCTCCCTTAAAA 720
DB 681 AGGCTGGACAAAGCAGGGGGCTACTTCTCCCTTCCCTGGGTCCAGTCTCCCTTAAAA 740
QY 721 GCGTGTGCAATTTTCCCTTCTCCCTTCTCCCTTCTCCCTTCTCCCTTCTCCCTTCTCC 780
DB 741 GCGTGTGCAATTTTCCCTTCTCCCTTCTCCCTTCTCCCTTCTCCCTTCTCCCTTCTCC 800
QY 781 TTAGGGAAGAGGATGTGGTCTCTGATCTGTGTGTCTCTGTGGTCTTTGGGGTGAAG 840
DB 801 TTAGGGAAGAGGATGTGGTCTCTGATCTGTGTGTCTCTGTGGTCTTTGGGGTGAAG 860
QY 841 GGATGGGGAAGGCGAGGCCAGAGGGGAATGGAGACATTCGAGGGGGCTCAGGAGTGAATG 900
DB 861 GGATGGGGAAGGCGAGGCCAGAGGGGAATGGAGACATTCGAGGGGGCTCAGGAGTGAATG 920
QY 901 CGATCTGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
DB 921 CGATCTGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 980
QY 961 TTACCTTGAAGATAAAGTGGGTCTTCAGGAACTCAGTGTCTGGGAGGAAAGCATGGC 1020
DB 981 TTACCTTGAAGATAAAGTGGGTCTTCAGGAACTCAGTGTCTGGGAGGAAAGCATGGC 1040
QY 1021 CAGGATTCAGGATGT 1080
DB 1041 CAGGATTCAGGATGT 1100
QY 1081 CAGGCTCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGG 1140
DB 1101 CAGGCTCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGG 1160
QY 1141 CCGCTTGAAGCTCAGTGGTCTTCAGGGTSCACTGGAAGCTGGTGTGGCTGTCCCTGTG 1200
DB 1161 CCGCTTGAAGCTCAGTGGTCTTCAGGGTSCACTGGAAGCTGGTGTGGCTGTCCCTGTG 1220
QY 1201 CACTTCTGGCACTGGGGCATGGAGTGGCCCATGCACTGCTGCTGGGTGCCCTCAGCTG 1260
DB 1221 CACTTCTGGCACTGGGGCATGGAGTGGCCCATGCACTGCTGCTGGGTGCCCTCAGCTG 1280
QY 1261 CACTTGAAGGCTGTGGCAGTCCCTCTCTCCCTGCTGCAAGTGTCCAGTGTGAGGCGAGG 1320
DB 1281 CACTTGAAGGCTGTGGCAGTCCCTCTCTCCCTGCTGCAAGTGTCCAGTGTGAGGCGAGG 1340
QY 1321 GTCGTTTGAACATGAGACTCGAGGCTGAGGCTGGAATCTGAACACCAAGCCCTGTACT 1380
DB 1341 GTCGTTTGAACATGAGACTCGAGGCTGAGGCTGGAATCTGAACACCAAGCCCTGTACT 1400
QY 1381 TGGGTTGCTCTGT 1440
DB 1401 TGGGTTGCTCTGT 1460
QY 1441 CTGTGTAGAGT 1499
DB 1461 CTGTGTAGAGT 1519

Db 1359 GTCGGTGGAAACATGAGACTCGAGGCTGAGGTGGATCTGGAACACACAGGCCCTGTAC 1418
Qy 1390 TTGGGTTGCCCTCTTTCCTGCACTTGGTTGTACCACTGATGAGAGAGAAAATTTTGTCC 1439
Db 1419 TTGGGTTGCCCTCTTTCCTGCACTTGGTTGTACCACTGATGAGAGAAAATTTTGTCC 1478
Qy 1440 TCTGTCTTAGAGTTGTGTAAATCAGAGAGCATCAATTAATGTTTATTTCCTC 1499
Db 1479 TCTGTCTTAGAGTTGTGTAAATCAGAGAGCATCAATTAATGTTTATTTCCTC 1538

RESULT 4

US-10-024-298A-150
; Sequence 150, Application US/10024298A
; Publication No. US20030143540A1
; GENERAL INFORMATION:
; APPLICANT: ASAHI KASEI KABUSHIKI KAISHA
; APPLICANT: AKIO MATSUDA
; APPLICANT: Goichi HONDA
; APPLICANT: Shuji MORAMATSU
; APPLICANT: Yukiko NAGANO
; TITLE OF INVENTION: NF-K B Activating Gene
; FILE REFERENCE: 1254-0191P
; CURRENT APPLICATION NUMBER: US/10/024,298A
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/314,385
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/278,641
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP254018/2001
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: JP0089912/2001
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP402288/2000
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 150
; LENGTH: 1562
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (120)..(668)
US-10-024-298A-150

Query Match 98.7%; Score 1480; DB 14; Length 1562;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1494; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
Qy 1 GCGGCTGCAGCGGGCTTTAGGTGTCCGGCTTTGCTGGCCAGCAAGCCTGATAGCATG 60
Db 63 GCGGCTGCAGCGGGCTTTAGGTGTCCGGCTTTGCTGGCCAGCAAGCCTGATAGCATG 122
Qy 61 AGGCTCTATCTTTGTTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 120
Db 123 AAGCTCTATCTTTGTTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 182
Qy 121 AAGGTTCTGAGATATCGGTGCAATGCAATCTGTCCACCTTATAGAAACATCAGTGG 180

Db 183 AAGGTTCTGAGATATCGGTGCAATGCAATCTGTCCACCTTATAGAAACATCAGTGG 242
Qy 181 CATATTACCAACAGAAATGTATCCAGAAAGGACTGCAGTGCCTGCTGAGAGGCC 240
Db 243 CACATTTACACACAGAAATGTATCCAGAAAGGACTGCAGTGCCTGCTGAGAGGCC 302
Qy 241 ATGCCAGTGGCTGGCCATGAGCTGAGAGGCTACTGCTGCTGTGGAGTGCAGTAAAG 300
Db 303 ATGCCAGTGGCTGGCCATGAGCTGAGAGGCTACTGCTGCTGTGGAGTGCAGTAAAG 362
Qy 301 GAGGCGACGACCAACCAACATCAAGTCAATGTGATCACTACCTGTCCGTGGTGG 360
Db 363 GAGGCGACGACCAACCAACATCAAGTCAATGTGATCACTACCTGTCCGTGGTGG 422
Qy 361 CTGTTGCTCTACATGSCCTTCCTGATGCTGGTGGAGCCCTCTGATCCGAAAGCCGATGCA 420
Db 423 CTGTTGCTCTACATGSCCTTCCTGATGCTGGTGGAGCCCTCTGATCCGAAAGCCGATGCA 482
Qy 421 TACACTGAGCAACTGCACATGAGGAGGAGATGAGATGCTGCTCTATGSCAGAGCT 480
Db 483 TATACTGAGCAACTGCACATGAGGAGGAGATGAGATGCTGCTCTATGSCAGAGCT 542
Qy 481 GCTGCATCCCTCGGGGAGCCCGAGCAACACAGTCTCTGAGAGGCTGTGGAAGTGGCCAG 540
Db 543 GCTGCATCCCTCGGGGAGCCCGAGCAACACAGTCTCTGAGAGGCTGTGGAAGTGGCCAG 602
Qy 541 CAGGGTGGAAAGCTGCAAGTGCAGGAGAGCAAGGAGAGACAGTCTTCGATCGGCAAGATG 600
Db 603 CAGGGTGGAAAGCTGCAAGTGCAGGAGAGCAAGGAGAGACAGTCTTCGATCGGCAAGATG 662
Qy 601 CTCAGCTAGATGGGTGGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 660
Db 663 CTCAGCTAGATGGGTGGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 722
Qy 661 AGGCTGCAGCAAAAGCAGGGGGCTACTTCTCCCTCCCTCGGTTCCAGTCTCCCTTTAAA 720
Db 723 AGGCTGCAGCAAAAGCAGGGGGCTACTTCTCCCTCCCTCGGTTCCAGTCTCCCTTTAAA 782
Qy 721 GCTGTGGCAATTTTCTCCTCTCTCCCTACTTTAGAAATGTTGATCTGGCTATTTGA 780
Db 783 GCTGTGGCAATTTTCTCCTCTCTCCCTACTTTAGAAATGTTGATCTGGCTATTTGA 842
Qy 781 TTAGGAGAGAGGATGGTGTCTGATCTCTGTGTCTCTTGGGCTTTGGGTTGAAG 840
Db 843 TTAGGAGAGAGGATGGTGTCTGATCTCTGTGTCTCTTGGGCTTTGGGTTGAAG 902
Qy 841 GGATGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900
Db 903 GGAGGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 962
Qy 901 GAGTGTCTCTGCTGGCTCCACTCTTCCGCGCTTCCAGCTCTGAGTCTTGGGAAATTTG 960
Db 963 GAGTGTCTCTGCTGGCTCCACTCTTCCGCGCTTCCAGCTCTGAGTCTTGGGAAATTTG 1022
Qy 961 TTACGCTTGGAGATTAAGCTGGGCTTTCAGAGACTCAGTGTCTGGGAGGAAAGCATGGC 1020
Db 1023 TTACGCTTGGAGATTAAGCTGGGCTTTCAGAGACTCAGTGTCTGGGAGGAAAGCATGGC 1082
Qy 1021 CCAGCATTCAGCATGTGTTCTTTTGTGCAAGTGGTTC-TTATCACCACTCCCTCCAGGCC 1079
Db 1083 CCAGCATTCAGCATGTGTTCTTTCTGCAAGTGGTTC-TTATCACCACTCCCTCCAGGCC 1142
Qy 1080 CCAGGCGCTCAGGCCCAAGCCCGCCAGCTCCAGGCTTCCAGGAGAGCTGTGATGGAGAGCTGG 1139

RESULT 5

Query Match	98.7%	Score 1480;	DB 14;	Length 1562;
Best Local Similarity	99.6%	Pred. No. 0;		

Query Match	98.7%	Score 1480;	DB 14;	Length 1562;
Best Local Similarity	99.6%	Pred. No. 0;		

Db 963 GAACTGTCTCTCTGGCTCCACTCTTGGCGCTTCAGCTCTGAGTCTTGGGAATGFG 1022
Qy 961 TTACCTTGGAAATAAGACTGGGTCTTCAGGAATCAGTGTCTGGGAGGAAAGCATGGC 1020
Db 1023 TTACCTTGGAAATAAGACTGGGTCTTCAGGAATCAGTGTCTGGGAGGAAAGCATGGC 1082
Qy 1021 CCAGATTCAGCATGTGTTCTTCTGAGTGTTC-TTATCACAACCTCCCTCCAGCC 1079
Db 1083 CCAGCATTCAGCATGTGTTCTTCTGAGTGTTC-TTATCACAACCTCCCTCCAGCC 1142
Qy 1080 CCAGCCCTCAGCCCAAGCCAGCTCCAGCCCTCAGGACAGCTCTGATGGAGAGCTGG 1139
Db 1143 CCAGCCCTCAGCCCAAGCCAGCTCCAGCCCTCAGGACAGCTCTGATGGAGAGCTGG 1202
Qy 1140 GCCCCTCAGCCCAAGCTGGGTCTTCAGGGTGCAGTGGAGAGCTGGTCTGCTGTCCCTGT 1199
Db 1203 GCCCCTCAGCCCAAGCTGGGTCTTCAGGGTGCAGTGGAGAGCTGGTCTGCTGTCCCTGT 1262
Qy 1200 GCATCTCTCAGCATGGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 1259
Db 1263 GCATCTCTCAGCATGGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 1322
Qy 1260 GCATCTGGGGGTCTGGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 1319
Db 1323 GCATCTGGGGGTCTGGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 1382
Qy 1320 GGTGGTGGAAATGAGTCTGGAGGCTGAGGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 1379
Db 1383 GGTGGTGGAAATGAGTCTGGAGGCTGAGGTGGAGTGGAGTGGAGTGGAGTGGAGTGG 1442
Qy 1380 TTGGGTGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1439
Db 1443 TTGGGTGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1502
Qy 1440 TCTGTCTTAGAGTTGTGTGAATCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1499
Db 1503 TCTGTCTTAGAGTTGTGTGAATCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1562

RESULT 6

US-10-153-668-93
; Sequence 93, Application US/10153668
; Publication No. US20030092616A1
; GENERAL INFORMATION:
; APPLICANT: HONDA, Goichi
; APPLICANT: MATSUDA, Akio
; APPLICANT: MURAMATSU, Shuji
; APPLICANT: ISHIZAWA, Kenya
; TITLE OF INVENTION: STAT6 Activating Gene
; FILE REFERENCE: 1254-0207P
; CURRENT APPLICATION NUMBER: US/10/153,668
; CURRENT FILING DATE: 2002-03-24
; PRIOR APPLICATION NUMBER: US 60/293,172
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/316,031
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/328,403
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: JP 2001-157043
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: JP 2001-260681
; PRIOR FILING DATE: 2001-08-30

; PRIOR APPLICATION NUMBER: JP 2001-313175
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 488
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 93
; LENGTH: 1503
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (63)...(611)
US-10-153-668-93

Query Match 98.6%; Score 1478; DB 14; Length 1503;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1492; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Qy 1 GCGGCTGCAGGGGCTTGTAGTGTCTGGGCTTGTCTGGCCAGAGAGCTGATAGCATG 60
Db 6 GCGGCTGCAGGGGCTTGTAGTGTCTGGGCTTGTCTGGCCAGAGAGCTGATAGCATG 65
Qy 61 AAGCTCTTATCTTGTGTGGCGTGTGGGTGTTTGTGTGGCGCCAGCTGAAGCAAC 120
Db 66 AAGCTCTTATCTTGTGTGGCGTGTGGGTGTTTGTGTGGCGCCAGCTGAAGCAAC 125
Qy 121 AAGAGTTCTGAAGATCCGGTGCAGATGATCTGTCCACCTTATAGAAACATCAGTGG 180
Db 126 AAGAGTTCTGAAGATCCGGTGCAGATGATCTGTCCACCTTATAGAAACATCAGTGG 185
Qy 181 CATATTACACACAGAAATGATCCAGAGAGACTGCAACTGCTGCACGTGTGGAGGCC 240
Db 186 CATATTACACACAGAAATGATCCAGAGAGACTGCAACTGCTGCACGTGTGGAGGCC 245
Qy 241 ATGCCAGTGGCTGGCCATGACGTGGAGGCTACTGCTGTGGAGAGTGCAGGTACAG 300
Db 246 ATGCCAGTGGCTGGCCATGACGTGGAGGCTACTGCTGTGGAGAGTGCAGGTACAG 305
Qy 301 GAGGCGACGACCAACCAACCAAGGTCTATCTGATCTACCTGTCCGTGTGGGTGCC 360
Db 306 GAGGCGACGACCAACCAACCAAGGTCTATCTGATCTACCTGTCCGTGTGGGTGCC 365
Qy 361 CTGTGTCTTACATGGCTTCCTGATGTGTGGTGGACCTCTGATCCGAAAGCCGATGCA 420
Db 366 CTGTGTCTTACATGGCTTCCTGATGTGTGGTGGACCTCTGATCCGAAAGCCGATGCA 425
Qy 421 TACACTGAGCAACTGCACATGAGGAGGAGTGGAGTGTCTCTATGGCAGAGCT 480
Db 426 TACTACTGAGCAACTGCACATGAGGAGGAGTGGAGTGTCTCTATGGCAGAGCT 485
Qy 481 GCTGATCCCTCGGGGGACCCCGAGCAACACAGTCTGTGGAGGCTGTGGAGTGGCCAG 540
Db 486 GCTGATCCCTCGGGGGACCCCGAGCAACACAGTCTGTGGAGGCTGTGGAGTGGCCAG 545
Qy 541 CAGCGGTGGAAGCTGCAGGTGAGGAGGAGGAGGAGTGTCTCTATGGCAGAGCT 600
Db 546 CAGCGGTGGAAGCTGCAGGTGAGGAGGAGGAGGAGTGTCTCTATGGCAGAGCT 605
Qy 601 CTCAGTAGATGGGTGTGTGGTGGGTCAAGGCCCCCAACCATGGCTGCCAGCTTCC 660
Db 606 CTCAGTAGATGGGTGTGTGGTGGGTCAAGGCCCCCAACCATGGCTGCCAGCTTCC 665
Qy 661 AAGCTGAGCAAGGAGGAGGAGTGTCTTCCCTGCGGTTCAGTCTCCCTTTTAAAA 720
|||||

RESULT 7
US-09-946-374-67
; Sequence 67, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc

APPLICANT:	Batch, Dan L.
APPLICANT:	Ferrara, Napoleone
APPLICANT:	Fong, Sherman
APPLICANT:	Gao, Wei-Qiang
APPLICANT:	Goddard, Audrey
APPLICANT:	Godowski, Paul J.
APPLICANT:	Grimaldi, Christopher J.
APPLICANT:	Gurney, Austin L.
APPLICANT:	Hillan, Kenneth J.
APPLICANT:	Pan, James
APPLICANT:	Paoni, Nicholas F.
APPLICANT:	Roy, Margaret Ann
APPLICANT:	Smith, Victoria
APPLICANT:	Stewart, Timothy A.
APPLICANT:	Tumas, Daniel
APPLICANT:	Watanabe, Colin K.
APPLICANT:	Williams, P. Mickey
APPLICANT:	Wood, William I.
TITLE OF INVENTION:	Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION:	Acids Encoding the Same
FILE REFERENCE:	P2830P1C1
CURRENT APPLICATION NUMBER:	US/09/946,374
CURRENT FILING DATE:	2001-09-04
PRIOR APPLICATION NUMBER:	60/098716
PRIOR FILING DATE:	1998-09-01
PRIOR APPLICATION NUMBER:	60/098723
PRIOR FILING DATE:	1998-09-01
PRIOR APPLICATION NUMBER:	60/098749
PRIOR FILING DATE:	1998-09-01
PRIOR APPLICATION NUMBER:	60/098750
PRIOR FILING DATE:	1998-09-01
PRIOR APPLICATION NUMBER:	60/098803
PRIOR FILING DATE:	1998-09-02
PRIOR APPLICATION NUMBER:	60/098821
PRIOR FILING DATE:	1998-09-02
PRIOR APPLICATION NUMBER:	60/098843
PRIOR FILING DATE:	1998-09-02
PRIOR APPLICATION NUMBER:	60/098936
PRIOR FILING DATE:	1998-09-09
PRIOR APPLICATION NUMBER:	60/098956
PRIOR FILING DATE:	1998-09-09
PRIOR APPLICATION NUMBER:	60/098958
PRIOR FILING DATE:	1998-09-09
PRIOR APPLICATION NUMBER:	60/098602
PRIOR FILING DATE:	1998-09-09
PRIOR APPLICATION NUMBER:	60/098642
PRIOR FILING DATE:	1998-09-09
PRIOR APPLICATION NUMBER:	60/098741
PRIOR FILING DATE:	1998-09-10
PRIOR APPLICATION NUMBER:	60/098754
PRIOR FILING DATE:	1998-09-10
PRIOR APPLICATION NUMBER:	60/098763
PRIOR FILING DATE:	1998-09-10
PRIOR APPLICATION NUMBER:	60/098792
PRIOR FILING DATE:	1998-09-10
PRIOR APPLICATION NUMBER:	60/098808
PRIOR FILING DATE:	1998-09-10
PRIOR APPLICATION NUMBER:	60/098812
PRIOR FILING DATE:	1998-09-10
PRIOR APPLICATION NUMBER:	60/098815
PRIOR FILING DATE:	1998-09-10
PRIOR APPLICATION NUMBER:	60/098816
PRIOR FILING DATE:	1998-09-10

7	PRIOR FILING DATE: 1998-09-24	
7	PRIOR APPLICATION NUMBER: 60/102207	
7	PRIOR FILING DATE: 1998-09-29	
7	PRIOR APPLICATION NUMBER: 60/102240	
7	PRIOR FILING DATE: 1998-09-29	
7	PRIOR APPLICATION NUMBER: 60/102307	
7	PRIOR FILING DATE: 1998-09-29	
7	PRIOR APPLICATION NUMBER: 60/102330	
7	PRIOR FILING DATE: 1998-09-29	
7	PRIOR APPLICATION NUMBER: 60/102331	
7	PRIOR FILING DATE: 1998-09-29	
7	PRIOR APPLICATION NUMBER: 60/102484	
7	PRIOR FILING DATE: 1998-09-30	
7	PRIOR APPLICATION NUMBER: 60/102487	
7	PRIOR FILING DATE: 1998-09-30	
7	PRIOR APPLICATION NUMBER: 60/102570	
7	PRIOR FILING DATE: 1998-09-30	
7	PRIOR APPLICATION NUMBER: 60/102571	
7	PRIOR FILING DATE: 1998-09-30	
7	PRIOR APPLICATION NUMBER: 60/102684	
7	PRIOR FILING DATE: 1998-10-01	
7	PRIOR APPLICATION NUMBER: 60/102687	
7	PRIOR FILING DATE: 1998-10-01	
7	PRIOR APPLICATION NUMBER: 60/102965	
7	PRIOR FILING DATE: 1998-10-02	
7	PRIOR APPLICATION NUMBER: 60/103258	
7	PRIOR FILING DATE: 1998-10-06	
7	PRIOR APPLICATION NUMBER: 60/103314	
7	PRIOR FILING DATE: 1998-10-07	
7	PRIOR APPLICATION NUMBER: 60/103315	
7	PRIOR FILING DATE: 1998-10-07	
7	PRIOR APPLICATION NUMBER: 60/103328	
7	PRIOR FILING DATE: 1998-10-07	
7	PRIOR APPLICATION NUMBER: 60/103395	
7	PRIOR FILING DATE: 1998-10-07	
7	PRIOR APPLICATION NUMBER: 60/103396	
7	PRIOR FILING DATE: 1998-10-07	
7	PRIOR APPLICATION NUMBER: 60/103401	
7	PRIOR FILING DATE: 1998-10-07	
7	PRIOR APPLICATION NUMBER: 60/103449	
7	PRIOR FILING DATE: 1998-10-06	
7	PRIOR APPLICATION NUMBER: 60/103633	
7	PRIOR FILING DATE: 1998-10-08	
7	PRIOR APPLICATION NUMBER: 60/103678	
7	PRIOR FILING DATE: 1998-10-08	
7	PRIOR APPLICATION NUMBER: 60/103679	
7	PRIOR FILING DATE: 1998-10-08	
7	PRIOR APPLICATION NUMBER: 60/103711	
7	PRIOR FILING DATE: 1998-10-08	
7	PRIOR APPLICATION NUMBER: 60/104257	
7	PRIOR FILING DATE: 1998-10-14	
7	PRIOR APPLICATION NUMBER: 60/104987	
7	PRIOR FILING DATE: 1998-10-20	
7	PRIOR APPLICATION NUMBER: 60/105000	
7	PRIOR FILING DATE: 1998-10-20	
7	PRIOR APPLICATION NUMBER: 60/105002	
7	PRIOR FILING DATE: 1998-10-20	
7	PRIOR APPLICATION NUMBER: 60/105104	
7	PRIOR FILING DATE: 1998-10-21	
7	PRIOR APPLICATION NUMBER: 60/105169	
7	PRIOR FILING DATE: 1998-10-22	
7	PRIOR APPLICATION NUMBER: 60/105266	
7	PRIOR FILING DATE: 1998-10-22	

; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807

Query Match 98.3%; Score 1473.6; DB 10; Length 1564;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1476; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 20 AGGTGTCGGGCTTTGGTGGCCCGAGAGCTGATAGATGAAGCTCTTATCTTTGGTGG 79
DB 84 AGGTGTCGGGCTTTGGTGGCCCGAGAGCTGATAGATGAAGCTCTTATCTTTGGTGG 143
QY 80 CGGTGTCGGGCTTTGGTGGCCCGAGAGCTGATAGATGAAGCTCTTATCTTTGGTGG 139
DB 144 CTGTGTCGGGCTTTGGTGGCCCGAGAGCTGATAGATGAAGCTCTTATCTTTGGTGG 203
QY 140 GGTGCAATGCACTGTCCCACTTATAGAAACATCACTGGGCAATATTACACCAAGATG 199
DB 294 GGTGCAATGCACTGTCCCACTTATAGAAACATCACTGGGCAATATTACACCAAGATG 263
QY 200 TATCCAGAGAGACTGCAACTGCTGCAAGTGGTGGAGCCCATGGCACTGCTGGCCATG 259
DB 264 TATCCAGAGAGACTGCAACTGCTGCAAGTGGTGGAGCCCATGGCACTGCTGGCCATG 323
QY 260 AGGTGAGGCTTACTGCTGCTGTGGAGGTGCAAGTACGAGAGAGAGAGAGAGAGAGAG 319
DB 324 AGGTGAGGCTTACTGCTGCTGTGGAGGTGCAAGTACGAGAGAGAGAGAGAGAGAGAG 383
QY 320 TCAAGTGCATCATGTTGATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 379
DB 384 TCAAGTGCATCATGTTGATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 443
QY 380 TCCTGATGCTGGTGGAGCTGCTGATCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 439
DB 444 TCCTGATGCTGGTGGAGCTGCTGATCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 503
QY 440 ATGAG 499
DB 504 ATGAG 563
QY 500 CCGAG 559
DB 564 CCGAG 623
QY 560 TCGAG 619
DB 624 TCGAG 683
QY 620 GTGGTGGTGAAGGCGCCAG 679
DB 684 GTGGTGGTGAAGGCGCCAG 743
QY 680 GCTACTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 739
DB 744 GCTACTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 803
QY 740 CTCTCTCCCTAATTTAGAAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 799
DB 804 CTCTCTCCCTAATTTAGAAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 863
QY 800 TCTCTGATCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 859

DB 864 TCTCTGATCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 923
QY 860 GAAGGGAATGAGACATTCGAGAGGCGCTCAGAGAGTGAATGGAATCTGTTCTCTCTGCT 919
DB 924 GAAGGGAATGAGACATTCGAGAGGCGCTCAGAGAGTGAATGGAATCTGTTCTCTCTG 983
QY 920 CACCTCTTGGCGCTTCCAGCTCTGAGTCTTGGGAATGTTGTTACCTTGGAGAAATG 979
DB 984 CACCTCTTGGCGCTTCCAGCTCTGAGTCTTGGGAATGTTGTTACCTTGGAGAAATG 1043
QY 980 CTGGGCTTTCAGAACTCAGTGTCTGGGAGGAAAGCATGGCCAGCATTCAGCATGTGTT 1039
DB 1044 CTGGGCTTTCAGAACTCAGTGTCTGGGAGGAAAGCATGGCCAGCATTCAGCATGTGTT 1103
QY 1040 CTTTCTGCACTGGTTCCTTATCACCACCTCCCTCCAGCCCAAGGCGCTCAGCCCAAGC 1099
DB 1104 CTTTCTGCACTGGTTCCTTATCACCACCTCCCTCCAGCCCAAGGCGCTCAGCCCAAGC 1163
QY 1100 CAGCTTCAGGCTCAG 1159
DB 1164 CAGCTTCAGGCTCAG 1223
QY 1160 CTTGAGGCTGCACTGAG 1219
DB 1224 CTTGAGGCTGCACTGAG 1283
QY 1220 TGAAGTGGCAATGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1279
DB 1284 TGAAGTGGCAATGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1343
QY 1280 GTCCCTCTCTCCCAAGTGTCCAGAGTCACTGAGGAGAGAGAGAGAGAGAGAGAGAGAG 1339
DB 1344 GTCCCTCTCTCCCAAGTGTCCAGAGTCACTGAGGAGAGAGAGAGAGAGAGAGAGAGAG 1403
QY 1340 TGAAGTGGCAATGCACTGAG 1399
DB 1404 TGAAGTGGCAATGCACTGAG 1463
QY 1400 GAAGTGGCTTACAGAGTGAAG 1459
DB 1464 GAAGTGGCTTACAGAGTGAAG 1523
QY 1460 TAATTCAG 1499
DB 1524 TAATTCAG 1563

RESULT 8

US-10-206-915-245
; Sequence 245, Application US/10206915
; Publication No. US20040029221A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.

```

/ APPLICANT: Zhang, Zemin.
/ TITLE OF INVENTION: ACIDS ENCODING THE SAME
/ FILE REFERENCE: P3430R1C3
/ CURRENT APPLICATION NUMBER: US/10/206,915
/ CURRENT FILING DATE: 2002-07-26
/ PRIOR APPLICATION NUMBER: 10/052586
/ PRIOR FILING DATE: 2002-01-15
/ PRIOR APPLICATION NUMBER: 60/059263
/ PRIOR FILING DATE: 1997-09-18
/ PRIOR APPLICATION NUMBER: 60/059266
/ PRIOR FILING DATE: 1997-09-18
/ PRIOR APPLICATION NUMBER: 60/062250
/ PRIOR FILING DATE: 1997-10-17
/ PRIOR APPLICATION NUMBER: 60/063120
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/063121
/ PRIOR FILING DATE: 1997-10-24
/ PRIOR APPLICATION NUMBER: 60/063486
/ PRIOR FILING DATE: 1997-10-21
/ PRIOR APPLICATION NUMBER: 60/063540
/ PRIOR FILING DATE: 1997-10-28
/ PRIOR APPLICATION NUMBER: 60/063541
/ PRIOR FILING DATE: 1997-10-28
/ PRIOR APPLICATION NUMBER: 60/063544
/ PRIOR FILING DATE: 1997-10-28
/ Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 612
/ SEQ ID NO 245
/ LENGTH: 1564
/ TYPE: DNA
/ ORGANISM: Homo Sapien
/ 10-206-915-245

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Query Match 98.3%; Score 1473.6; DB 12; Length: 1564;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1476; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

[illegible]

QY 1340 TCGAGCTGACGGTGGATCTGAACACACAGAGCCCTGACTGGTGGCTCTGTGCTT 1399
Db 1404 TCGAGCTGACGGTGGATCTGAACACACAGAGCCCTGACTGGTGGCTCTGTGCTT 1463
QY 1400 GAATCTGCTGTACCACTGATGGAGAGAAATTTTGTCTCTGTCTTAGAGTGTG 1459
Db 1464 GAATCTGCTGTACCACTGATGGAGAGAAATTTTGTCTCTGTCTTAGAGTGTG 1523
QY 1460 TAAATCAAGAGAGCCATTAATTAATTTTATTTCTCTC 1499
Db 1524 TAAATCAAGAGAGCCATTAATTAATTTTATTTCTCTC 1563

RESULT 9

US-10-199-670-245
; Sequence 245, Application US/10199670
; Publication No. US20040033560A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P430R1C401
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 245
; LENGTH: 1564
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-199-670-245

Query Match 98.3%; Score 1473.6; DB 12; Length 1564;

Best Local Similarity 99.7%; Pred. No. 0;
Matches 1476; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 20 AGGTGTCCGGCTTTGCTGGCCACAGAGCTCATTAAGCATGAAGCTCTTATCTTTGGG 79
Db 84 AGGTGTCCGGCTTTGCTGGCCACAGAGCTCATTAAGCATGAAGCTCTTATCTTTGGG 143
QY 80 CCGTGTGGGTGTGCTGGTGGCCACAGAGCTGAAGCCAAAGAGTTCTGAAGATATCC 139
Db 144 CTGTGTGGGTGTGCTGGTGGCCACAGAGCTGAAGCCAAAGAGTTCTGAAGATATCC 203
QY 140 GGTGCAATGCACTGTCCACCTTATAGAAACATCATGTGGGCAATTTTACACAGATG 199
Db 204 GGTGCAATGCACTGTCCACCTTATAGAAACATCATGTGGGCAATTTTACACAGATG 263
QY 200 TATCCAGAGGAGCTGCACCTGCTGCAGGTGGTGGAGCCCATGCCAGTGGCCATG 259
Db 264 TATCCAGAGGAGCTGCACCTGCTGCAGGTGGTGGAGCCCATGCCAGTGGCCATG 323
QY 260 ACSTGGAGGGCTACTGCTGCTGTGGAGTGCAGGTACGAGAGGAGGAGACACACCA 319
Db 324 ACSTGGAGGGCTACTGCTGCTGTGGAGTGCAGGTACGAGAGGAGGAGACACACCA 383
QY 320 TCAAGGTCACTCATTTGTCACTACCTGCTGGTGGTGGTGGCTGTCTACATGGCT 379
Db 384 TCAAGGTCACTCATTTGTCACTACCTGCTGGTGGTGGTGGCTGTCTACATGGCT 443
QY 380 TCCTGATGCTGGTGGACCTCTGATCCGAAAGCCGGATGCAATACATGAGCAACTGCACA 439
Db 444 TCCTGATGCTGGTGGACCTCTGATCCGAAAGCCGGATGCAATACATGAGCAACTGCACA 503
QY 440 ATGAGAGAGAGATGAGATGCTGCTCTATGGCAGAGCTGCTGCATCCCTCGGGGAC 499
Db 504 ATGAGAGAGAGATGAGATGCTGCTCTATGGCAGAGCTGCTGCATCCCTCGGGGAC 563
QY 500 CCGGAGCAAAACACAGTCTGTGAGAGTGGCAGAGTGGCAGAGGCTGAGAGCTGAGG 559
Db 564 CCGGAGCAAAACACAGTCTGTGAGAGTGGCAGAGTGGCAGAGGCTGAGAGCTGAGG 623
QY 560 TCGAGAGAGAGTGGAGAGAGTCTTGGATCGGCAAGATGCTCAGCTAGATGGCTGGT 619
Db 624 TCGAGAGAGAGTGGAGAGAGTCTTGGATCGGCAAGATGCTCAGCTAGATGGCTGGT 683
QY 620 GTGGTGGGTCAAGGCCCCACACAGTGGCTGGCAGCTCCAGGCTGAGCAAGAGGGG 679
Db 684 GTGGTGGGTCAAGGCCCCACACAGTGGCTGGCAGCTCCAGGCTGAGCAAGAGGGG 743
QY 680 GCTACTTCTCCCTTCCCTGGTCCAGTCTTCCCTTTAAAGCTGTGGCATTTCCTC 739
Db 744 GCTACTTCTCCCTTCCCTGGTCCAGTCTTCCCTTTAAAGCTGTGGCATTTCCTC 803
QY 740 CTCTCCCTTAACCTTAGAAATGTTGACTTGGCTATTTGATTAGGAGAGAGGATGG 799
Db 804 CTCTCCCTTAACCTTAGAAATGTTGACTTGGCTATTTGATTAGGAGAGAGGATGG 863
QY 800 TCTCTGATCTCTGTCTCTCTGGGTCTTTGGGTTGAGGATGGGAGAGGAGGAGGCA 859
Db 864 TCTCTGATCTCTGTCTCTCTGGGTCTTTGGGTTGAGGAGAGGAGGAGGAGGAGGCA 923
QY 860 GAAGGAGATGAGAGATTCAGAGGCGGCTCAGAGTGGATGGATCTCTCTCTGGCT 919
Db 924 GAAGGAGATGAGAGATTCAGAGGCGGCTCAGAGTGGATGGATCTCTCTCTGGCT 983

[illegible]

Query Match 98.3%; Score 1473.6; DB 12; Length 1564;

QY	80	CCGTGGTTCGGGTTGTTTCTGCTGGTGCCCAAGCTGAAGCCAAACAGAGTTCTGAAGATATCC	133
DB	144	CTTGTGTGGGGTGTGTTGCTGGTGGCCCAAGCTGAAGCCAAACAGAGTTCTGAAGATATCC	203
QY	140	GGTGCAAATGCACTCTGTCCACCTTATAGAAACATCAGTGGGCAATTTTACAAACAGAGTG	199
DB	204	GGTGCAAATGCACTCTGTCCACCTTATAGAAACATCAGTGGGCAATTTTACAAACAGAGTG	263
QY	200	TATCCAGAAAGAACTGCACCTGCTGTGCAAGTGGTGGAGCCCAATGCCAGTGGCTGGCAATG	259
DB	264	TATCCAGAAAGAACTGCACCTGCTGTGCAAGTGGTGGAGCCCAATGCCAGTGGCTGGCAATG	323
QY	260	ACGTGGAGGCTACTGGCTGTGTGTGGAGGACAGGATACAGGAGCGGACGACACACACCA	319
DB	324	ACGTGGAGGCTACTGGCTGTGTGTGGAGGACAGGATACAGGAGCGGACGACACACACCA	383
QY	320	TCAAGTCAATCAATGTCACTCACTGTCCGTGGTGGGTGGCTGTTGCTCAATGGCT	379
DB	384	TCAAGTCAATCAATGTCACTCACTGTCCGTGGTGGGTGGCTGTTGCTCAATGGCT	443
QY	380	TCCGTGATGCTGGTGGACCTCTGATCCGAAGCCGGATGCATCACTGAGCACTGCACA	439
DB	444	TCCGTGATGCTGGTGGACCTCTGATCCGAAGCCGGATGCATCACTGAGCACTGCACA	503
QY	440	ATGAGAGAGAGATGAGATGCTGCTCTATATGGCAAGCTGCTGCATCCCTCGGGAGAC	499
DB	504	ATGAGAGAGAGATGAGATGCTGCTCTATATGGCAAGCTGCTGCATCCCTCGGGAGAC	563
QY	500	CCGAGCAAAACAACGCTCTGAGCGGTGAGAGGTGCCACAGCGGTGAGAGCTGCAGG	559
DB	564	CCGAGCAAAACAACGCTCTGAGCGGTGAGAGGTGCCACAGCGGTGAGAGCTGCAGG	623
QY	560	TGCAGAGCAACGGAAGACAGTCTTCGATCGGCAAGAATGCTCAGCTAGATGGGTGGT	619
DB	624	TGCAGAGCAACGGAAGACAGTCTTCGATCGGCAAGAATGCTCAGCTAGATGGGTGGT	683
QY	620	GTGGTGGGTCAAGGCCCAACACCAATGAGCTGCACAGCTTCCAGGCTGAGCAAAACAGAGG	679
DB	684	GTGGTGGGTCAAGGCCCAACACCAATGAGCTGCACAGCTTCCAGGCTGAGCAAAACAGAGG	743
QY	680	GCTACTCTCCCTCCGTTCCAGTCTTCCAGTCTTCCCTTAAAGCCTGTGGCATTTTCTCTC	739
DB	744	GCTACTCTCCCTCCGTTCCAGTCTTCCAGTCTTCCCTTAAAGCCTGTGGCATTTTCTCTC	803
QY	740	CTTCTCCCTCAACTTAAAGATGTTGACTTCGCTATTTGATTAGGGAAGAGGGATGTGG	799
DB	804	CTTCTCCCTCAACTTAAAGATGTTGACTTCGCTATTTGATTAGGGAAGAGGGATGTGG	863
QY	800	TCTCTGACTCTGTTGTTCTCTTGGGTCTTTGGGGTTGAAGGGAATGGGAGGCAAGCA	859
DB	864	TCTCTGACTCTGTTGTTCTCTTGGGTCTTTGGGGTTGAAGGGAATGGGAGGCAAGCA	923
QY	860	GAAGGGAATGGAGACATTCGAGCGGCTCAGGAGTGGATGGATCTGTCTCTCTGGCT	919
DB	924	GAAGGGAATGGAGACATTCGAGCGGCTCAGGAGTGGATGGATCTGTCTCTCTGGCT	983
QY	920	CCACTCTTGGCGCTTCCAGCTCTGAGTCTTGGGAATGTTTACCTTGGAGATAAAG	979
DB	984	CCACTCTTGGCGCTTCCAGCTCTGAGTCTTGGGAATGTTTACCTTGGAGATAAAG	1043
QY	980	CTGGGTCTTCAGAACTCAGTGTCTGGGAGGAAGCATGGCCCAAGCATCAGCATGTGTT	1039
DB	1044	CTGGGTCTTCAGAACTCAGTGTCTGGGAGGAAGCATGGCCCAAGCATCAGCATGTGTT	1103

RESULT 12

US-10-208-C24-245

Sequence 245, Application US/10208024

Publication No. US20040048335A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Chen, Jian

APPLICANT: Desnoyers, Luc

APPLICANT: Goddard, Audrey

7. APPLICANT: Godowski, Paul

APPLICANT: Gurney, Austin

APPLICANT: Pan, James

APPLICANT: Smith, Victoria

APPLICANT: Watanabe, Colin

APPLICANT: Wood, William I

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRET

FILE OF INVENTION: ACIDS
FILE REFERENCE: P3430R1C53

FILE REFERENCE: F3430K1C35

CURRENT FILING DATE: 2002

PRIOR APPLICATION NUMBER:

PRIOR FILING DATE: 2002-01

PRIOR APPLICATION NUMBER:

PRIOR FILING DATE: 1997-09

10 PRIOR APPLICATION NUMBER:

PRIOR FILING DATE: 1997-09

;; PRIOR APPLICATION NUMBER:

: PRIOR FILING DATE: 1997-10


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, PRIOR APPLICATION NUMBER: 60/063120
, PRIOR FILING DATE: 1997-10-24
, PRIOR APPLICATION NUMBER: 60/063121
, PRIOR FILING DATE: 1997-10-24
, PRIOR APPLICATION NUMBER: 60/063486
, PRIOR FILING DATE: 1997-10-21
, PRIOR APPLICATION NUMBER: 60/063540
, PRIOR FILING DATE: 1997-10-28
, PRIOR APPLICATION NUMBER: 60/063541
, PRIOR FILING DATE: 1997-10-28
, PRIOR APPLICATION NUMBER: 60/063544
, PRIOR FILING DATE: 1997-10-28
, Prior Application data removed - See
, NUMBER OF SEQ ID NOS: 612
, SEQ ID NO 245
, LENGTH: 1564
, TYPE: DNA
, ORGANISM: Homo sapien
US-10-208-024-245

```

Query Match 98.3%; Score 1473.6; DB 12; Length 1564;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1476; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY	20	AGTGTTCGGGCTTGGCTGGCCGACGAAGGCTGATGACATGAAGCTCTTATCTTTGGTGG	79
Db	84	AGTGTTCGGGCTTGGCTGGCCGACGAAGGCTGATGACATGAAGCTCTTATCTTTGGTGG	143
QY	80	CCGTGTTCGGGTGTTTGGTGGTCCGCCACAGCTGAAGCCACACAGAGTTCTGAGATATCC	139
Db	144	CTGTGTGGGGTGTTCGTGGTGGCCGCCACAGCTGAAGCCACACAGAGTTCTGAAGATATCC	203
QY	140	GGTGCAAAATGCATCTGTCCACCTTTATAGAAAACATCAGTGGGCATATTACACACCAAGT	199
Db	204	GGTGCAAAATGCATCTGTCCACCTTTATAGAAAACATCAGTGGGCACANTTACACACAGATG	263
QY	200	TATCCGACAGAGGACTGGAATCTGCTGCACGTGGTGGAGCCCAATGCCAGTGGCTGGCCATG	259
Db	264	TATCCGACAGAGGACTGGAATCTGCTGCACGTGGTGGAGCCCAATGCCAGTGGCTGGCCATG	323
QY	260	ACGTGGAGGCGCTACTGGCTGCTGTGGAGGTGCAGGTACGAGAGCGGCAGCGACCAACACCA	319
Db	324	ACGTGGAGGCGCTACTGGCTGCTGTGGAGGTGCAGGTACGAGAGCGGCAGCGACCAACACCA	383
QY	320	TCAAGTGCATCAATGTGCATCTAAGTGTCCGTGGTGGTGGCTGCTTACATAGGCT	379
Db	384	TCAAGTGCATCAATGTGCATCTAAGTGTCCGTGGTGGTGGCTGCTTACATAGGCT	443
QY	380	TGCTGTGATGCTGGTGGACGCTCTGATCCGAAAGCCGAGATGATACATGAGAGACTGCAC	439
Db	444	TGCTGTGATGCTGGTGGACGCTCTGATCCGAAAGCCGAGATGATACATGAGAGACTGCAC	503
QY	440	ATGAGCAGAGATGAGGATGCTCCGTCTATGGCAGCAGCTGCTGCATCCCTCGGGGGAC	499
Db	504	ATGAGCAGAGATGAGGATGCTCCGTCTATGGCAGCAGCTGCTGCATCCCTCGGGGGAC	563
QY	500	CCCGAGCAAAACACAGTCTCTGGAGCGCTGTGGAAGTGCACAGCAGCGGTGGAGCTGCA	559
Db	564	CCCGAGCAAAACACAGTCTCTGGAGCGCTGTGGAAGTGCACAGCAGCGGTGGAGCTGCA	623
QY	560	TGCAGAGCAGCGGAGAGACAGTCTTCGATCGGCAAGATGCTCAGCTAGTGGGCTGTGT	619
Db	624	TGCAGAGCAGCGGAGAGACAGTCTTCGATCGGCAAGATGCTCAGCTAGTGGGCTGTGT	683

RESULT: 13

Db 1164 CCAGCTCCAGCCCTGAGGACAGCTCTGATGGGAGGAGCTGGGCCCCCTGAGCCACATGGGT 1223
Qy 1160 CTTACGGGTGACGAGCTGAGTGTTCCTGTCCCTGTGCACTTTCCGACTGGGCA 1219
Db 1224 CTTACGGGTGACGAGCTGAGTGTTCCTGTGCACTTTCCGACTGGGCA 1283
Qy 1220 TGGAGTGGCCATGATACCTCTGCTGCCGGTCCCTCACTTGAAGGCTGGGCA 1279
Db 1284 TGGAGTGGCCATGATACCTCTGCTGCCGGTCCCTCACTTGAAGGCTGGGCA 1343
Qy 1280 GTCCCTCTCTCCCACTGTCACAGTCTGACAGAGGCTGGGTTGGAACATGAGAC 1339
Db 1344 GTCCCTCTCTCCCACTGTCACAGTCTGACAGAGGCTGGGTTGGAACATGAGAC 1403
Qy 1340 TGGAGTGGCCATGATACCTCTGACAGAGGCTGTACTTGGGTTGCTCTGTGTCCT 1399
Db 1404 TGGAGTGGCCATGATACCTCTGACAGAGGCTGTACTTGGGTTGCTCTGTGTCCT 1463
Qy 1400 GAACTCTGTTGACAGTGCATGGAGAGAAATTTGTCTCTGTCTAGAGTTGTGTG 1459
Db 1464 GAACTCTGTTGACAGTGCATGGAGAGAAATTTGTCTCTGTCTAGAGTTGTGTG 1523
Qy 1460 TAAATCAGGAAGCCATCAATTAATTTTTCCTC 1499
Db 1524 TAAATCAGGAAGCCATCAATTAATTTTTCCTC 1563

RESULT 14

US-10-052-586-245
; Sequence 245, Application US/10052586
; Publication No. US20020127584A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C1
; CURRENT APPLICATION NUMBER: US/10/052,586
; CURRENT FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541

; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063564
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063734
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063870
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066120
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/066466
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066772
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/069335
; PRIOR FILING DATE: 1997-12-11
; PRIOR APPLICATION NUMBER: 60/069425
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: 60/069870
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/068017
; PRIOR FILING DATE: 1997-12-16
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/078896
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
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; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
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; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
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; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081838
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082569
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22

7	PRIOR APPLICATION NUMBER: 60/082719	
7	PRIOR FILING DATE: 1998-04-22	
7	PRIOR APPLICATION NUMBER: 60/083322	
7	PRIOR FILING DATE: 1998-04-28	
7	PRIOR APPLICATION NUMBER: 60/083495	
7	PRIOR FILING DATE: 1998-04-29	
7	PRIOR APPLICATION NUMBER: 60/083496	
7	PRIOR FILING DATE: 1998-04-29	
7	PRIOR APPLICATION NUMBER: 60/083499	
7	PRIOR FILING DATE: 1998-04-29	
7	PRIOR APPLICATION NUMBER: 60/083559	
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7	PRIOR APPLICATION NUMBER: 60/083466	
7	PRIOR FILING DATE: 1998-05-05	
7	PRIOR APPLICATION NUMBER: 60/084414	
7	PRIOR FILING DATE: 1998-05-06	
7	PRIOR APPLICATION NUMBER: 60/084639	
7	PRIOR FILING DATE: 1998-05-07	
7	PRIOR APPLICATION NUMBER: 60/084640	
7	PRIOR FILING DATE: 1998-05-07	
7	PRIOR APPLICATION NUMBER: 60/084643	
7	PRIOR FILING DATE: 1998-05-07	
7	PRIOR APPLICATION NUMBER: 60/085573	
7	PRIOR FILING DATE: 1998-05-15	
7	PRIOR APPLICATION NUMBER: 60/085579	
7	PRIOR FILING DATE: 1998-05-15	
7	PRIOR APPLICATION NUMBER: 60/085580	
7	PRIOR FILING DATE: 1998-05-15	
7	PRIOR APPLICATION NUMBER: 60/085582	
7	PRIOR FILING DATE: 1998-05-15	
7	PRIOR APPLICATION NUMBER: 60/085700	
7	PRIOR FILING DATE: 1998-05-15	
7	PRIOR APPLICATION NUMBER: 60/086023	
7	PRIOR FILING DATE: 1998-05-18	
7	PRIOR APPLICATION NUMBER: 60/086392	
7	PRIOR FILING DATE: 1998-05-22	
7	PRIOR APPLICATION NUMBER: 60/086486	
7	PRIOR FILING DATE: 1998-05-22	
7	PRIOR APPLICATION NUMBER: 60/087098	
7	PRIOR FILING DATE: 1998-05-28	
7	PRIOR APPLICATION NUMBER: 60/087268	
7	PRIOR FILING DATE: 1998-05-28	
7	PRIOR APPLICATION NUMBER: 60/087609	
7	PRIOR FILING DATE: 1998-06-02	
7	PRIOR APPLICATION NUMBER: 60/087759	
7	PRIOR FILING DATE: 1998-06-02	
7	PRIOR APPLICATION NUMBER: 60/087827	
7	PRIOR FILING DATE: 1998-06-03	
7	PRIOR APPLICATION NUMBER: 60/088025	
7	PRIOR FILING DATE: 1998-06-04	
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7	PRIOR APPLICATION NUMBER: 60/088033	
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7	PRIOR APPLICATION NUMBER: 60/088167	
7	PRIOR FILING DATE: 1998-06-05	
7	PRIOR APPLICATION NUMBER: 60/088202	
7	PRIOR FILING DATE: 1998-06-05	
7	PRIOR APPLICATION NUMBER: 60/089212	
7	PRIOR FILING DATE: 1998-06-05	
7	PRIOR APPLICATION NUMBER: 60/089217	

Db 324 ACCTGGAGGCGCTACTGGCTGCTGTGGAGTGCAGTACGAGAGCGGACGACACCA 383
QY 320 TCAAGGTCAITCATTTGTCATCACTGTCCTGCTGGTGGTGGCTGTTGCTCTACATGGCT 379
Db 384 TCAAGGTCAITCATTTGTCATCACTGTCCTGCTGGTGGTGGCTGTTGCTCTACATGGCT 443
QY 380 TCCGTGATGCTGGTGGACCTCTGATCCGAAAGCGGGATGCATACACTGAGCACTGACCA 439
Db 444 TCCGTGATGCTGGTGGACCTCTGATCCGAAAGCGGGATGCATACACTGAGCACTGACCA 503
QY 440 ATGAGGAGGAGATGAGATGCTGGCTCTATGGCAGGAGCTGCTGCATCCCTCGGGGAC 499
Db 504 ATGAGGAGGAGATGAGATGCTGGCTCTATGGCAGGAGCTGCTGCATCCCTCGGGGAC 563
QY 500 CCCGAGCAAAACAACAGTCTGGAGGCTGTGGAGGTGCCAGACAGGGGTGGAGCTGACAG 559
Db 564 CCCGAGCAAAACAACAGTCTGGAGGCTGTGGAGGTGCCAGACAGGGGTGGAGCTGACAG 623
QY 560 TGCAGGAGCAGGGAGAGAGCTCTGATCGGACAGATGCTCAGCTAGATGGCTGGT 619
Db 624 TGCAGGAGCAGGGAGAGAGCTCTGATCGGACAGATGCTCAGCTAGATGGCTGGT 683
QY 620 GTGGTTGGGTCAAGGCCCCAACACACATGGCTGCCAGCTTCCAGGCTGGACAAAGCAGGG 679
Db 684 GTGGTTGGGTCAAGGCCCCAACACACATGGCTGCCAGCTTCCAGGCTGGACAAAGCAGGG 743
QY 680 GCTACTCTCCCTCCCTCGGTCCAGTCTTCCCTTAAAGGCTGGGCACTTTTCCTC 739
Db 744 GCTACTCTCCCTCCCTCGGTCCAGTCTTCCCTTAAAGGCTGGGCACTTTTCCTC 803
QY 740 CTTCTCCCTAACTTAAAGTGTGTACTTGGCTATTTGATAGGAGAGGGATGG 799
Db 804 CTTCTCCCTAACTTAAAGTGTGTACTTGGCTATTTGATAGGAGAGGGATGG 863
QY 800 TCTCTGATCTGTTCTCTCTGGGTCTTTGGGGTTGAAGGGATGGGAGGCAAGGCA 859
Db 864 TCTCTGATCTGTTCTCTCTGGGTCTTTGGGGTTGAAGGGATGGGAGGCAAGGCA 923
QY 860 GAAGGAGATGGACATTCGAGGCGGCTCAGGAGTGGATGGATGCTCTCTCTGGCT 919
Db 924 GAAGGAGATGGACATTCGAGGCGGCTCAGGAGTGGATGGATGCTCTCTCTGGCT 983
QY 920 CCACTCTTGGCGCTTCCAGCTCTGAGTCTTGGGAATGTTGTACCTTGGAAATAAAG 979
Db 984 CCACTCTTGGCGCTTCCAGCTCTGAGTCTTGGGAATGTTGTACCTTGGAAATAAAG 1043
QY 980 CTGGGTCTTCAAGGACTCAGTGTCTGGAGGAAAGCATGGCCACAGATTCAGCATGTGT 1039
Db 1044 CTGGGTCTTCAAGGACTCAGTGTCTGGAGGAAAGCATGGCCACAGATTCAGCATGTGT 1103
QY 1040 CTTTCTGAGTGGTCTTTATCAGACCTCCCTCCAGCCCGGCTCAGGCCAGCC 1099
Db 1104 CTTTCTGAGTGGTCTTTATCAGACCTCCCTCCAGCCCGGCTCAGGCCAGCC 1163
QY 1100 CCAAGCTCCAGCCCTGAGGACAGCTCTGATGGGAGAGTGGGCCCCCTGAGCCACTGGGT 1159
Db 1164 CCAAGCTCCAGCCCTGAGGACAGCTCTGATGGGAGAGTGGGCCCCCTGAGCCACTGGGT 1223
QY 1160 CTTCAAGGTGACATGGAGAGTGGTGTGGCTGTCCCTGTGCACTTCTGGCACTGGGCA 1219
Db 1224 CTTCAAGGTGACATGGAGAGTGGTGTGGCTGTCCCTGTGCACTTCTGGCACTGGGCA 1283
QY 1220 TGGAGTGGCCATGCATCTCTGCTGGGGTCCCTCAGCTGCACTTGGGGGTCTGGCA 1279

Db 1284 TGAAGTGGCCATGCATCTGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 1343
QY 1280 GTCCCTCCCTCTCCCCAGTGTCCACAGTCACTGAGCCAGAGGCTGGTGGAAACATGAGAC 1339
Db 1344 GTCCCTCCCTCTCCCCAGTGTCCACAGTCACTGAGCCAGAGGCTGGTGGAAACATGAGAC 1403
QY 1340 TGAAGTGGAGCTGGATCTGACACACAGGCCCCCTGACTGGGGTGGCTCTTGGCTCT 1399
Db 1404 TGAAGTGGAGCTGGATCTGACACACAGGCCCCCTGACTGGGGTGGCTCTTGGCTCT 1463
QY 1400 GAAGTGGCTGTACAGTGCATGGAGAGAAATTTGCTCTCTGCTTAGAGTTGGTG 1459
Db 1464 GAAGTGGCTGTACAGTGCATGGAGAGAAATTTGCTCTCTGCTTAGAGTTGGTG 1523
QY 1460 TAAATCAAGGAGCCATCATTAATTTGTTTATTTCTCTC 1499
Db 1524 TAAATCAAGGAGCCATCATTAATTTGTTTATTTCTCTC 1563

RESULT 15

US-10-174-590-245
; Sequence 245, Application US/10174590
; Publication No. US20030008352A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430RIC42
; CURRENT APPLICATION NUMBER: US/10/174,590
; CURRENT FILING DATE: 2002-06-18
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 245
; LENGTH: 1564
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-174-590-245

Query Match 98.3%; Score 1473.6; DB 14; Length 1564;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1476; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 20 AGGTGTCCGGCTTGTGCTGGCCAGCAAGCTGATAAGCATGAAGCTCTATCTTTGGTGG 79
Db 84 AGGTGTCCGGCTTGTGCTGGCCAGCAAGCTGATAAGCATGAAGCTCTATCTTTGGTGG 143
QY 80 CGGTGGTGGTGTGCTGGTGGCCCGAGCTGAAGCCACAGAGTTCTGAAGATATCC 139
Db 144 CTGTGGTGGTGTGCTGGTGGCCCGAGCTGAAGCCACAGAGTTCTGAAGATATCC 203
QY 140 GGTGAATGCATCTGCACTTATAGAAACATCACTGGGCATATTTACACCAAGATG 199

Db	1164	CGAGCTTCAGGCCCTGAGGACAGCTCTGATGGGAGAGCTGGGCCGCCCTGAGCCACCTGGGGT	1223
Qy	1160	CTTCAGGGTGCACCTGGAAAGCTGGTGTTCGTGTCCCTGTGCACATCTCGACATGGGGCA	1219
Db	1224	CTTCAGGGTGCACCTGGAAAGCTGGTGTTCGTGTCCCTGTGCACATCTCGACATGGGGCA	1283
Qy	1220	TGGAGTGGCCCATGCATATCTGCTGCCGGTCCCTGCACCTGACATGAGGGGTCTGGGCA	1279
Db	1284	TGGAGTGGCCCATGCATATCTGCTGCCGGTCCCTGCACCTGACATGAGGGGTCTGGGCA	1343
Qy	1280	GTCCCTTCCTCTCCCCAGTGTCCACAGTCACATGAGCCACAGCGGTGGTTGGAAACATGAGAC	1339
Db	1344	GTCCCTTCCTCTCCCCAGTGTCCACAGTCACATGAGCCACAGCGGTGGTTGGAAACATGAGAC	1403
Qy	1340	TCGAGGCTGAGGCTGATCTGATCCTGACACACAGCCCTGTACTTGGTTCCTCTTGTGTCCT	1399
Db	1404	TCGAGGCTGAGGCTGATCTGATCCTGACACACAGCCCTGTACTTGGTTCCTCTTGTGTCCT	1463
Qy	1400	GAACTTCGTTGTACAGTGGCATGGAGAGAAAATTTTTCCTCTTGTCTTACAGTTCGTGG	1459
Db	1464	GAACTTCGTTGTACAGTGGCATGGAGAGAAAATTTTTCCTCTTGTCTTACAGTTCGTGG	1523
Qy	1460	TAAATCAAGGAAGCCATCAATTAATTTATTTATCTC	1499
Db	1524	TAAATCAAGGAAGCCATCAATTAATTTATTTATCTC	1563

Search completed: April 4, 2004, 00:36:12
Job time : 365.216 secs

OM nucleic - nucleic search, using sw model

Run on: April 3, 2004, 01:46:51 ; Search time 2536.04 Seconds
(without alignments)
17650.880 Million cell updates/sec

Title: US-10-030-269A-1
Perfect score: 1499
Sequence: 1 gcggctgcagcggctgtgta.....taaatgtttttttttttc 1499

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:**

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estnu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_htc:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_htc:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: em_gss_hum:*
- 18: em_gss_inv:*
- 19: em_gss_pin:*
- 20: em_gss_vit:*
- 21: em_gss_fun:*
- 22: em_gss_man:*
- 23: em_gss_mus:*
- 24: em_gss_pro:*
- 25: em_gss_red:*
- 26: em_gss_phg:*
- 27: em_gss_vrl:*
- 28: gb_gss1:*
- 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1480	98.7	1592	11	AF151020	AF151020 Homo sapi
2	1391.4	72.8	1201	13	EX356220	EX356220 EX356220
3	1324.8	68.4	1201	13	EX356219	EX356219 EX356219
4	1017.2	67.9	1221	9	AL563840	AL563840 AL563840
5	1002	66.8	1201	9	AL530793	AL530793 AL530793
6	992.6	66.2	1201	13	EX341787	EX341787 EX341787
7	977.8	65.2	1201	13	EX419772	EX419772 EX419772
8	963.6	64.3	1139	9	AL515384	AL515384 AL515384
9	952.8	63.6	1201	9	AL528644	AL528644 AL528644
10	947	63.2	1095	13	EX341455	EX341455 EX341455
11	938.2	62.6	1201	9	AL572900	AL572900 AL572900
12	925.2	61.7	1201	9	AL514307	AL514307 AL514307
13	923.8	61.6	1201	9	AL563216	AL563216 AL563216
14	916.6	61.1	1201	13	EX334438	EX334438 EX334438
15	912	60.8	1201	13	EX340039	EX340039 EX340039
16	911.6	60.8	1030	13	EX394372	EX394372 EX394372
17	903.2	60.3	1201	13	EX334437	EX334437 EX334437
18	901.2	60.1	1201	9	AL514308	AL514308 AL514308
19	897.2	59.9	1017	13	EX394373	EX394373 EX394373
20	896.8	59.8	1201	13	EX341788	EX341788 EX341788
21	894.2	59.7	1201	9	AL548272	AL548272 AL548272
22	890	59.4	977	13	EX399479	EX399479 EX399479
23	869.2	58.0	918	13	EX406847	EX406847 EX406847
24	867.2	57.9	1124	13	EX360008	EX360008 EX360008
25	851	56.8	1201	13	EX393741	EX393741 EX393741
26	834	55.6	1201	13	EX342010	EX342010 EX342010
27	833.6	55.6	893	9	AL561955	AL561955 AL561955
28	831.2	55.5	881	9	AL582044	AL582044 AL582044
29	831	55.4	934	9	AL520688	AL520688 AL520688
30	830.4	55.4	908	13	EX406848	EX406848 EX406848
31	829.6	55.3	923	9	AL521080	AL521080 AL521080
32	829.4	55.3	907	13	EX392869	EX392869 EX392869
33	824.8	55.0	914	13	EX453077	EX453077 AGENCOURT
34	811.6	54.1	933	13	EX957082	EX957082 AGENCOURT
35	808	53.9	1158	9	AL516745	AL516745 AL516745
36	801.8	53.5	935	13	EX948426	EX948426 AGENCOURT
37	799.4	53.3	875	9	AL560630	AL560630 AL560630
38	797.6	53.2	946	9	AL520687	AL520687 AL520687
39	797.4	53.2	1159	13	EX333999	EX333999 EX333999
40	789.4	52.7	1201	13	EX342009	EX342009 EX342009
41	779.6	52.0	931	13	EX541471	EX541471 AGENCOURT
42	775	51.7	944	13	EX399478	EX399478 EX399478
43	769.8	51.4	944	13	EX501879	EX501879 AGENCOURT
44	767.8	51.2	868	14	CD048308	CD048308 AGENCOURT
45	756	50.4	893	13	EX434912	EX434912 EX434912

ALIGNMENTS

RESULT 1
AF151020
LOCUS AF151020 1592 bp mRNA linear HTC 22-MAY-2001
DEFINITION Homo sapiens HSPC186 mRNA, complete cds.
ACCESSION AF151020
VERSION AF151020.1 GI:7106761
KEYWORDS HTC.

OM nucleic - nucleic search, using sw model

Run on: April 3, 2004, 00:09:01 ; Search time 4698.38 Seconds
(without alignments)
16863.481 Million cell updates/sec

Title: US-10-030-269A-3
Perfect score: 1828
Sequence: 1 aagcgacgcttcgcccctc.....ctattttaagtcacatcagct 1828

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 2167516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl: *
1: gb_ba: *
2: gb_htg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vi: *
15: em_ba: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_mu: *
20: em_om: *
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Search completed: April 3, 2004, 16:37:15
Job time : 2552.24 secs

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 35: em_htg_rnd:**
 36: em_htg_man:**
 37: em_htg_vrt:**
 38: em_sy:**
 39: em_htgo_hum:**
 40: em_htgo_mus:**
 41: em_htgo_other:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1828	100.0	1828	6	AX136217 Sequence
2	1828	100.0	1828	6	BD093295 Anyfold b
3	1828	100.0	1828	6	BD123561 Secretory
4	1828	100.0	1828	9	AK075438 Homo sapi
5	1502.6	82.2	200557	9	AC009052 Homo sapi
6	1499.4	82.0	141208	2	AP001492 Homo sapi
7	1499.4	82.0	195637	2	AP002420 Homo sapi
8	1499.4	82.0	217873	9	HUAC004382
9	966	47.4	64365	2	AC009089 Homo sapi
10	582.8	31.9	677	6	AX136524 Sequence
11	582.8	31.9	677	6	BD123764 Secretory
12	453.2	24.8	474	6	AX136667 Sequence
13	453.2	24.8	474	6	BD123907 Secretory
14	391.4	21.4	1639	9	BC054340 Homo sapi
15	241.6	13.2	1717	10	BC036386 Mus muscu
16	133	7.3	235915	10	AC129606
17	131	7.2	194290	2	AC137228 Rattus no
18	131	7.2	194317	2	AC137232
19	131	7.2	256944	2	AC096512 Rattus ro
20	72.4	4.0	191745	5	AL929303 Zebrafish
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23	63	3.4	168922	9	AP002007 Homo sapi
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45	54.6	3.0	114540	9	AC107426 Homo sapi

ALIGNMENTS

RESULT 1	AX136217	Sequence 139 from Patent EP1067182.	1828 bp	DNA	linear	PAT 30-MAY-2001
LOCUS	AX136217					
DEFINITION	AX136217	Sequence 139 from Patent EP1067182.				
ACCESSION	AX136217					
VERSION	AX136217.1	GI:14272625				
KEYWORDS						
SOURCE						
ORGANISM						
	Homo sapiens					
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	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE						
AUTHORS	Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.					
TITLE	Secretory protein or membrane protein					
JOURNAL	Patent: EP 1067182-A 139 10-JAN-2001;					
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Qy	61	GGGGGAGCTGGCCGCTTCCAAATGGGGCGGGCGGTATCTGGTGGCGTTGGCGGCGG	120			
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Qy	121	GGGCTGGAGGCTCTGCAGCTGGATGGCTGGCGTGGCGGCTGGCGGCTGGCGGCTGGT	180			
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DEFINITION	Anyloid beta aglication regulatory factor.				
ACCESSION	BD093295				
VERSION	BD093295.1	GI:22638683			
KEYWORDS	WO 0104299-A/2.				
SOURCE	human				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 1828)				
AUTHORS	Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Yamazaki,M., Sato,S., Arakawa,H. and Morita,M.				
TITLE	Anyloid beta aglication regulatory factor				
JOURNAL	Patent: WO 0104299-A 2 18-JAN-2001; HELIX RESEARCH INSTITUTE,TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA, YURI KAWAI,MAYAKO YAMAZAKI,SUSUMU SATO,HIROYUKI ARAKAWA, MASASHIKO MORITA				
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	PD	18-JAN-2001			

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D _b	1081	GAGTTGCATCTTCCTCCAGGCTTCGTGCGAGGGCACTACCATGGACATGGGCAAGG	1140
Q _y	1141	TTGCTGCTTTACTGAATTTAACTGTTATTTCTCTCTCTCTCACTCCCAAGTGCACCA	1200
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Q _y	1201	TTTGGTAACAGAGTCTCATTTAGTGAATGTGGGTGCTGTGACTTCACATGTAGGCTCAT	1260
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PF 06-JUL-2000 WO 2000JP004515
 PR 08-JUL-1999 JP 99P 194179,18-OCT-1999 US 60/159586 PI
 TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, YURI KAWAI, MAYAKO PI
 YAMAZAKI.
 PI SUSUKU SATO, HIROKUKI ARAKAWA, MASAHITO MORITA
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QY 1 AAGGAGACGTTGGCCCTCTTAGGGCCGTGGTCCCGTAGCTACCGGTGGCGTGGCGGT 60
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LOCUS
DEFINITION Secretory protein or membrane protein.
ACCESSION BD123561
VERSION BD123561.1 GI:23218506
KEYWORDS JP 2002017376-A/70.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1828)
AUTHORS Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and
Hayashi,K.
TITLE Secretory protein or membrane protein
JOURNAL Patent: JP 2002017376-A 70 22-JUN-2002;
HELIX RESEARCH INSTITUTE
COMMENT OS Homo sapiens (human)
PN JP 2002017376-A/70
PD 22-JUN-2002
PF 07-JUL-2000 JP 2002053173
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PI SUGIYAMA,
PI KOJI HAYASHI
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LOCUS AK075438 1828 bp mRNA linear PRI 03-SEP-2002

DEFINITION Homo sapiens cDNA PSEC0129 fls, clone PLACE100470.

ACCESSION AK075438

VERSION AK075438.1 GI:22761526

KEYWORDS oligo capping; fls (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 Ota,T., Nishikawa,T., Suzuki,Y., Kawai-Hio,Y., Hayashi,K., Ishii,S., Saito,K., Yamamoto,J., Wakamatsu,A., Nagai,T., Nakamura,Y., Nagahara,K., Sugano,S. and Isogai,T.

HRI human cDNA sequencing project

Unpublished

2 (bases 1 to 1828)

Isogai,T. and Yamamoto,J.

Direct Submission

Submitted (20-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

HRI human cDNA sequencing project; cDNA 5'- & 3'-end one pass sequencing, clone selection and full insert sequencing; Helix Research Institute (supported by Japan Key Technology Center etc.); cDNA library construction; Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center.

FEATURES

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DB 61 GGGCGACGCTGCGCGCTTCGCAAAATGGCGCGCGCGGGGATCTGCTGGCTTCGGCGGGC 120

QY 121 GGGCTGGAGGCTCCTGCAGCTGGATGCTGCGCGCTGGCGCGCTTCGCGACAGCGCTGCT 180

DB 121 GGGCTGGAGGCTCCTGCAGCTGGATGCTGCGCGCTGGCGCGCTTCGCGACAGCGCTGCT 180

QY 181 GCGCGCTGCTTCCATGCTTCAGCTGTGGGGCTAAGGCTTTCAGTACGACGACGACGAC 240

DB 181 GCGCGCTGCTTCCATGCTTCAGCTGTGGGGCTAAGGCTTTCAGTACGACGACGACGAC 240

QY 961 TTTTCTGCTAGTACAGCTGCTGCTTTAGATTAGGCGAGGCTCATGTTTCAGGCGAT 1020

DB 961 TTTTCTGCTAGTACAGCTGCTGCTTTAGATTAGGCGAGGCTCATGTTTCAGGCGAT 1020

QY 1021 GTTGTAGAGATCTCCAGCATAGCAATACCATCTCTCCAGAGACTGAGGGGATGACA 1080

DB 1021 GTTGTAGAGATCTCCAGCATAGCAATACCATCTCTCCAGAGACTGAGGGGATGACA 1080

QY 1081 GAGTTGCACTCTCCATCCAGGCTTCTCCAGGCGCATCTACCATGGACATGGGCAAG 1140

DB 1081 GAGTTGCACTCTCCATCCAGGCTTCTCCAGGCGCATCTACCATGGACATGGGCAAG 1140

QY 1141 TTCTGCTTACTGAATTAATGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1200

DB 1141 TTCTGCTTACTGAATTAATGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1200

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RESULT 4

AK075438

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QY 301 AGAGTCTTCTCATTACCCGCCAGATATACAGACAGGGGCGCGAGGAGAGGAGACTA 360
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QY 361 TGAAGTGAAGGAGGAGTGCAGAGACCGCACTCTGAAGGAGCGCTTGAAGTGTGCGCGC 420
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Db 1801 AAGAGAGAGTATTTTAAAGTACATCAGT 1828

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Job time : 4705.59 secs

OM nucleic - nucleic search, using sw model

Run on: April 2, 2004, 21:47:00 ; Search time 457.958 Seconds
(without alignments)
16957.243 Million cell updates/sec

Title: US-10-C30-269A-3
Perfect score: 1828
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1828	100.0	1828	4	AAF29358
2	1828	100.0	1828	5	AAF93813
3	1502.6	82.2	28149	5	ABAI7961
4	1499.4	82.0	10425	5	ABAI7962
5	1499.4	82.0	32192	5	ABAI7963
6	582.8	31.9	677	5	AAF94012
7	457.4	25.0	1835	3	AAC76921
8	453.2	24.8	474	5	AAF94155
9	432.4	23.7	1672	7	ABX63154
10	393.2	21.5	1652	4	AAS22866
11	391.4	21.4	1672	4	AAS22630
12	380.8	20.8	1290	6	ABK49891

13	374.8	20.5	2692	5	AAAF29358
14	372.8	20.4	1825	5	AAS65051
15	227.2	12.4	345	7	ABX48511
16	206.2	11.3	486	8	ACH14840
17	200	10.9	570	8	ACH14441
18	171	9.4	465	4	AAI15633
19	171	9.4	465	4	AAI15633
20	171	9.4	465	4	ABA57650
21	171	9.4	465	4	AAI37217
22	171	9.4	465	4	ABA27068
23	171	9.4	465	4	AAK31322
24	171	9.4	465	4	AAK05704
25	171	9.4	465	4	ABS31003
26	165.8	9.1	169	4	ABS06074
27	165.8	9.1	169	4	AAI24858
28	165.8	9.1	169	4	AAI50406
29	165.8	9.1	169	4	ABA36985
30	165.8	9.1	169	4	AAK44411
31	165.8	9.1	169	4	AAK18498
32	165.8	9.1	169	4	ABS44068
33	165.8	9.1	169	6	ABS18646
34	117.4	6.4	904	5	AAS65050
35	98.2	3.2	21082	5	ABAI7928
36	98.2	3.2	21087	5	ABAI7927
37	51.6	2.8	31129	6	AAD36229
38	51.2	2.8	1041	6	ABS61503
39	51	2.8	186591	7	ACF62750
40	51	2.8	186591	7	ADB20869
41	51	2.8	186591	9	ADB87958
42	51	2.8	186591	9	ADB96941
43	51	2.8	186591	9	ADB92132
44	51	2.8	208643	7	ACF62735
45	51	2.8	208643	7	ACF62740

ALIGNMENTS

RESULT 1
AAF29358
ID AAF29358 standard; DNA; 1828 BP.
XX
AC AAF29358;
XX
XX
DT 20-APR-2001 (first entry)
XX
DE Human; amyloid-beta protein agglutination regulating factor DNA SEQ ID 3.
XX
KW Human; amyloid-beta protein; agglutination regulatory factor;
KW Alzheimer's disease; ds.
XX
XX Homo sapiens.
XX
XX W0200104299-A1.
XX
XX
PD 18-JAN-2001.
XX
PF 06-JUL-2000; 2000WO-JP004515.
XX
XX
PR 08-JUL-1999; 99JP-00194179.
PR 18-OCT-1999; 99US-015986P.
XX
XX (HELI-) HELIX RES INST.
PA

XX Ota T, Isegai T, Nishikawa T, Kawai Y, Yamazaki M, Satoh S;
PI Arakawa H, Morita M;
XX WPI: 2001-139347/14.
XX Polynucleotide encoding Amyloid-beta protein agglutination-controlling
DK factor, useful for inhibiting or promoting agglutination or sedimentation
PT of amyloid-beta protein and in diagnosis and screening drugs for
PT Alzheimer's disease.
XX Claim 1: Page 46-48; 72pp; Japanese.
PS This invention relates to polynucleotides AAF29357 - AAF29361 which
XX encode proteins AAB49767 - AAB49771. The proteins inhibit or promote the
CC agglutination of amyloid beta protein. The protein and polynucleotide
CC sequences are useful in the diagnosis of Alzheimer's disease. They are
CC also useful for screening drugs which are useful for treating Alzheimer's
CC disease
XX Sequence 1828 BP; 497 A; 409 C; 437 G; 485 T; 0 U; 0 Other;
SQ

Query Match 100.0%; Score 1828; DB 4; Length 1828;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1828; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGACGAGCTTCGGCCCTCTTAGGGCCCTGGTCCCGTAGCTACCGGTGCGGTGCGCGT 60
DB 1 AAGGACGAGCTTCGGCCCTCTTAGGGCCCTGGTCCCGTAGCTACCGGTGCGGTGCGCGT 60

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DB 601 CAATAGGTTGGAACCTGGCTTTATTATTATTATTATTATTATTATTATTATTATTATTATTATT 660
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OM nucleic - nucleic search, using sw model

Run on: April 3, 2004, 11:14:53 ; Search time 439.276 Seconds
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15564.412 Million cell updates/sec

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Gapop 10.0, Gapext 1.0

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	432.4	23.7	1672	13	US-10-044-C90-154	Sequence 154, App
4	393.2	21.5	1652	15	US-10-291-263-668	Sequence 668, App

5	391.4	21.4	1672	15	US-10-291-263-196	Sequence 196, App
6	371.4	20.3	1649	14	US-10-102-524-1792	Sequence 1792, App
7	227.2	12.4	345	9	US-09-960-352-13676	Sequence 13676, A
8	206.2	11.3	486	10	US-09-918-993-2052	Sequence 2052, App
9	201.2	11.0	792	13	US-10-027-632-165754	Sequence 165754, A
10	200	10.9	570	10	US-09-918-993-28653	Sequence 28653, A
11	199.6	10.9	663	15	US-10-027-632-292346	Sequence 292346, A
12	171	9.4	465	9	US-09-864-761-5534	Sequence 5534, App
13	165.8	9.1	169	9	US-09-864-761-22305	Sequence 22305, A
c 14	51.6	2.8	3129	14	US-10-298-192-3	Sequence 3, Appli
c 15	51.2	2.8	1041	14	US-10-000-256A-111	Sequence 111, App
c 16	50.6	2.8	1380	14	US-10-000-256A-112	Sequence 112, App
c 17	50.6	2.8	1654	9	US-09-764-864-66	Sequence 66, Appli
c 18	48.2	2.6	341	15	US-10-027-632-94351	Sequence 94351, A
c 19	48.2	2.6	341	13	US-10-027-632-318428	Sequence 318428, A
c 20	47.4	2.6	5673	9	US-09-782-378A-17	Sequence 17, Appli
c 21	47.2	2.6	579	15	US-10-027-632-83792	Sequence 83792, A
c 22	47.2	2.6	3673778	14	US-10-312-841-2	Sequence 2, Appli
c 23	46.6	2.5	13737	11	US-09-900-448-3	Sequence 3, Appli
c 24	46.6	2.5	64467	14	US-10-274-409-3	Sequence 175, App
c 25	46.2	2.5	5908	12	US-10-221-613-175	Sequence 93, Appli
c 26	46.2	2.5	5908	14	US-10-239-676-93	Sequence 105, App
c 27	46.2	2.5	5908	14	US-10-240-453-105	Sequence 2085, App
c 28	46	2.5	7624	14	US-10-311-455-2385	Sequence 45, Appli
c 29	46	2.5	139095	12	US-10-017-128-3	Sequence 690, App
c 30	46	2.5	191395	12	US-10-235-192A-45	Sequence 220, App
c 31	45.8	2.5	12007	14	US-10-311-455-690	Sequence 1716, App
c 32	45.8	2.5	19576	12	US-10-221-613-220	Sequence 233933, A
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c 34	45.6	2.5	529	15	US-10-027-632-233933	Sequence 1919, App
c 35	45.6	2.5	1058	15	US-10-027-632-233934	Sequence 93113, A
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c 39	44.8	2.5	605	15	US-10-027-632-93114	Sequence 46465, A
c 40	44.8	2.5	605	15	US-10-027-632-93115	Sequence 46466, A
c 41	44.2	2.4	611	15	US-10-027-632-242304	Sequence 2126, App
c 42	43.8	2.4	597	15	US-10-027-632-46465	Sequence 588, App
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Job time : 445.276 secs

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Run on: April 3, 2004, 01:46:51 ; Search time 3092.65 Seconds
(without alignments)
17650.880 Million cell updates/sec

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Perfect score: 1828
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Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

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5	412.4	22.6	666	12	BG747410	BG747410 602704895
6	406.4	22.2	751	12	BE1762409	BE1762409 603049088
7	405.8	22.2	513	10	BE266566	BE266566 601193557
8	405.6	22.2	692	14	CD244298	CD244298 AGENCOURT
9	401.8	22.0	712	12	BI596364	BI596364 603243091
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18	394	21.6	596	9	AV702496	AV702496 AV702496
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33	385	21.1	901	13	BK421483	BK421483 BX421483
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OM nucleic - nucleic search, using sw model

Run on: April 3, 2004, 00:09:01 ; Search time 4071.25 Seconds
(without alignments)
16863.481 Million cell updates/sec

Title: JS-10-030-269A-5
Perfect score: 1584
Sequence: 1 ggcgtccgcgcgtgcact.....ataaagattattaaaccacc 1584

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Gapop 10.0 , Gapext 1.0

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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7	1577.2	99.6	1726	6	AX701352	AX701352 Sequence
8	1573.2	99.3	1702	6	E38394	E38394 Wnt-6 polyp
9	1573.2	99.3	1702	9	AY009401	AY009401 Homo sapi
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11	1447.2	91.4	1432	9	AB059570	AB059570 Homo sapi
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23	520	32.8	526	6	BD123820	BD123820 Secretary
24	512	32.3	512	6	AR220904	AR220904 Sequence
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26	415.6	26.2	228187	2	AC127107	AC127107 Rattus no
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ALIGNMENTS

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 VERSION AX136323.1 GI:14272729
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 Ota, T., Isogai, T., Nishikawa, T., Kawai, Y., Sugiyama, T. and
 AUTHORS Hayashi, K.
 TITLE Secretory protein or membrane protein
 JOURNAL Patent: EP 1067182-A 245 10-JAN-2001;
 Helix Research Institute (JP)
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ORIGIN

Query Match 100.0%; Score 1584; DB 6; Length 1584;
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1561	DB	AT	CAATAAAGATATTAAACACC	1584

RESULT 2	BD093296	1584 bp	linear	PAT 27-AUG-2002
LOCUS	BD093296			
DEFINITION	Amyloid beta aglification regulatory faccer.			
ACCESSION	BD093296			
VERSION	BD093296.1	GI:22638884		
KEYWORDS	WO C104299-A/3.			
SOURCE	Homo sapiens (human)			

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1594)

AUTHORS	Ota, T., Isogai, T., Nishikawa, T., Kawai, Y., Yamazaki, M., Sato, S., Arakawa, H. and Morita, M.
TITLE	Amyloid beta aggregation regulatory factor
JOURNAL	Patent: WO 0104299-A 3 18-JAN-2001; HELIIX RESEARCH INSTITUTE, TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, YURI KAWAI, MAYAKO YAMAZAKI, SUSUMU SATO, HIROYUKI ARAKAWA, MASAHITO MORITA

COMMENT	OS	Homo sapiens (human)
	PN	WC 0104/239-A/3
	FD	13-JAN-2001
	FF	06-JUL-2000 WC 2000JF004515
	PR	08-JUL-1999 JP 99P 1941/9, 18-OCT-1999 US 60/159586 PI
		TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, YURI KAWAI, MAYAKO PI
		YAMAZAKI,
	PI	SUSUMU SATO, HIROYUKI ARAKAWA, MASAHIKO MORITA
	PC	C12N15/12, C07K16/18, C12N5/10, A61K45/00, A61K48/00, PC
		A61K31/711,
	PC	A61P25/28, G01N33/15, G01N33/50
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	FH	Key
	FT	Location/Qualifiers
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FEATURES	Location/Qualifiers
1. <i>Location</i>	
2. <i>Qualifiers</i>	
3. <i>Other</i>	

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Db	841	GCGGGCTGCTGGAGGGCTTCGACGGCGCTCACCGCTCATGGSCACCAACAGCGCGAAG	900
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Db	961	CGCGATTGGCCCGGACTTGGGCGCCGAAACGGACGACCGGGCTCCCCGGGACGCGGGGT	1020
Qy	1021	CGGCGCTGCATACGAGCGCGCGGACTCAGCGGCTGGCACTCTGCTGTGCTGGCGCGCG	1080
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QY	481	GAGCTGCTGACGTGAGGCTGCGACAGCGGCCCGCTGGGGGGCGCCCTCCCGGGCGCTCCGGC	540
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QY	601	CAGTGGGGAGAGGCTGGGGGAGGACGTGGACTTCGGGAGCAGAGCTGAGAGCTCTTTATG	660
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QY	661	GAGCGCGGCGACAGCGGGACCGCGAGACATCGCGCGGTTGGTCAACTGCAACAACAG	720
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QY	721	GAGCGCGGCGACGGCTGGCGTGGCGAGCGACACCGCGGACCGAGTGCMAATGCAACGGCGTG	780
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DB	961	GCGGATTCGCGCGACTCTGGGCGCCCAACGAGCGACCGGCTCCCGGGCAGCGCGGT	1020
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DB	1261	CACCGGCAACCGGGCGCTTCGCGCGTTCGAGCGCGACGCGCTCTCGTGCMAAGGCCATCTC	1320
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DB	1321	CAGGGGCTCTGAAATGGTGAGGCGGGGCTTGAGAGGAGCGCCACCCACCGAGAGGCC	1380

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LOCUS	Homo sapiens cDNA PSEC0220 fis,				
DEFINITION	similar to Mouse Wnt-6 mRNA.				

ACCESSION	AK075522
VERSION	AK075522.1
KEYWORDS	oligo capping; fls (full insert sequence).
SOURCE	Homio sapiens (human)
ORGANISM	Homio sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

1
REFERENCE
AUTHORS
Ota, T., Nishikawa, T., Suzuki, Y., Kawai-Hio, Y., Hayashi, K.,
Ishii, S., Saito, K., Yanamoto, J., Wakamatsu, A., Nagai, T.,
Nakamura, Y., Nagehara, K., Sugano, S. and Isogait, T.

TITLE HRI human cDNA sequencing project
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1584)
 AUTHORS Isocai,T. and Yamamoto,J.

TITLE
JOURNAL
Direct Submission
Submitted (20-MAR-2002) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1332-3 Yana, Kisarazu, Chiba 292-0812, Japan
[E-mail: genomics@hri.co.jp, Tel: 01-438-52-3975, Fax: 01-438-52-5986]

COMMENT

HRI human cDNA sequencing project; cDNA 5'- & 3'-end one pass sequencing, clone selection and full insert sequencing; Helix Research Institute (supported by Japan Key Technology Center etc.); cDNA library construction; Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genom Center.

FEATURES	Location/Qualifiers
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ORIGIN

Query Match 100.0%; Score 1584; DB 9; Length 1584;
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Matches 1584; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1561 ATCAATAAAGATATTAAACACC 1584

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AX565675
LOCUS AX565675 1726 bp DNA linear PAT 29-NOV-2002
DEFINITION Sequence 36 from Patent W002077204.
ACCESSION AX565675

VERSION AX565675.1 GI:26000994

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 Andrews, P., Walsh, J., and Gokhale, P.

AUTHORS Stem cell

TITLE Patent: WO 02077204-A 36 03-OCT-2002;

JOURNAL Aordia Limited (GB)

FEATURES

source Location/Qualifiers

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ORIGIN

Query Match 99.6%; Score 1577.2; DB 6; Length 1726;

Best Local Similarity 99.8%; Pred. No. 1e-212;

Matches 1579; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 1505 GCGGCGGCGGCTTCCAGGCGGCTTCCAGGCGGCTTCCAGGCGGCTTCCAGGCGG 1564

QY 1441 CTGCGGCGGCGGCTTCCAGGCGGCTTCCAGGCGGCTTCCAGGCGGCTTCCAGGCGG 1500

DB 1565 CTGCGGCGGCGGCTTCCAGGCGGCTTCCAGGCGGCTTCCAGGCGGCTTCCAGGCGG 1624

QY 1501 GCGGCTGCTGAGGCGCTTCCAGGCGGCTTCCAGGCGGCTTCCAGGCGGCTTCCAG 1560

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[illegible][illegible]

Ds	1505	AGGGGCCACAGACGGGCCCCGAAAAAGCGGCTCTGGGGAGAGGCTTTAAAGGAGGAGCTGTACAGGCC	1566
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Ds	1565	CTCCCTCCCTTCCTGGCTCTAGAGAGGAAACAGTTTTTTAGACTGGAAAAAGCCAGCTAA	1624
Qy	1501	AGGCTCTGGATCTGGGCTCCCGAGACTGCTGGGCGACAGGATGGTGGGTGAGGTAGT	1560
Ds	1625	AGGCTCTGGATCTGGGCTCCCGAGACTGCTGGGCGACAGGATGGTGGGTGAGGTAGT	1684
Qy	1561	ATCAATTAAGATATTTTAAACCA	1582
Ds	1685	ATCAATTAAGATATTTTAAACCA	1706
RESULT 7			
LOCUS	AX701352	Sequence 21 from Patent WO03012082.	1726 bp DNA linear PAT 03-APR-2003
DEFINITION	AX701352		
ACCESSION	AX701352		
VERSION	AX701352.1	GI:29537001	
KEYWORDS			
SOURCE		Homo sapiens (human)	
ORGANISM		Homo sapiens	
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1		
AUTHORS	Andrews P., Walsh J. and Gokhale P.		
TITLE	Method for modulating stem cell differentiation using stem loop rna		
JOURNAL	Patent: WO 03012082-A 21 13-FEB-2003;		
	Axordia Limited (US)		
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Query Match	99.6%	Score 1577.2; DB 6; Length 1726;	
Best Local Similarity	99.8%	Pred. No. 1e-212;	
Matches 1579; Conservative	0; Mismatches 3; Indels 0; Gaps 0;		
Qy	1	GGGCTCGGGCGCTCGGACCTGAAGCCCGGGCCCTCGGGCGGGCGGCTTGGCGCCGAGCC	60
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Qy	61	TGGCCCTCTGCCACCCGGGCGGGCTAGGGCGGTACGATGCTGGCGCCCTTACCTCC	120
Ds	185	TGGCCCTCTGCCACCCGGGCGGGCTAGGGCGGTACGATGCTGGCGCCCTTACCTCC	244
Qy	121	CGGCTCGGGCTGCTGCTGTGCTGTCTGTGTGGCGGCGGAGCTGGCGGAGCTGTGGTGG	180
Ds	245	CGGCTCGGGCTGCTGCTGTGCTGTCTGTGTGGCGGCGGAGCTGGCGGAGCTGTGGTGG	304
Qy	181	GCTGTGGGCGACCCCTTGGTATGAGCCCTACAGCATCTGCAGGAAGCGAGCGGGCTG	240
Ds	305	GCTGTGGGCGACCCCTTGGTATGAGCCCTACAGCATCTGCAGGAAGCGAGCGGGCTG	364
Qy	241	GCCGGGGCGAGCGCGAGTGTGGCAGGCTTGAGCGGAGTGGTGGCGAGAGCTAGCTCGG	300
Ds	365	GCCGGGGCGAGCGCGAGTGTGGCAGGCTTGAGCGGAGTGGTGGCGAGAGCTAGCTCGG	424
Qy	301	GGGCGCCCGGCTGGGGGTTGCAAGAGTGCAAGTTCAGATTCGCTTCGGCGCTTGGATTCG	360

Db	425	GGCGCCCGCGCTCGGGGTGGAGAGTGCAGTTCACAGTTCGGCTTCGCGCTCGCGCTGGAATGCG	484
Qy	361	TCGAGCCACAGCAAGGCGTTTGGACGATCCTTGCAACAGGACATTCGCGGAGACGCGCTTC	420
Db	485	TCGAGCCACAGCAAGGCGTTTGGACGATCCTTGCAACAGGACATTCGCGGAGACGCGCTTC	544
Qy	421	GTGTTCGCATCATCTGGCGCGCGGCGCAGCGCGCTGACGCGAGTCTGTCTCTATGGGCG	480
Db	545	GTGTTCGCATCATCTGGCGCGCGGCGCAGCGCGCTGACGCGAGTCTGTCTCTATGGGCG	604
Qy	481	GAGCTGCTGCAGTGGGCTGCCAAGCGCGCCCGCTGGCGGCGCCCTTCGCGGCGCTTC	540
Db	605	GAGCTGCTGCAGTGGGCTGCCAAGCGCGCGCGCGCGCGCGCTTCGCGGCGCTTC	664
Qy	541	CTGCGCGGCGATCCCGGAGACCCCTGTGGCGCGCGCGCGCTTCGCGGCGCGCGCTTC	600
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Qy	601	GAGTGGGAGGCTCGCGACGACCTGGACTTCGGGGACAGAGTGGAGGCTCTTTATG	660
Db	725	GAGTGGGAGGCTCGCGACGACCTGGACTTCGGGGACAGAGTGGAGGCTCTTTATG	784
Qy	661	GAGCGCGGCACAGCGGGGCGCGGAGATCCCGCGGTTGGTGCACATCTGCACAACAC	720
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Qy	841	GCGCGCGCTGTGAGCGCTTCACAGCGCGCTTCACCGGCTCATGGGCAACACAGCGCGAG	900
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Qy	901	GCCTGTGTCGCGCGTCCGCAAGCTCAAAGCGCGCGCGGAGCGGAGCTTCCTCATAGCGC	960
Db	1025	GCCTGTGTCGCGCGTCCGCAAGCTCAAAGCGCGCGCGGAGCGGAGCTTCCTCATAGCGC	1084
Qy	961	GCGATTTCGCGCGACTTCTGGCGCGCCAAACCGACGCAACCGGCTTCGCGCGCGCGGCT	1020
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Db	1145	CGCGCTTCGAATAGCAGCGCGCGGAGCTCATAGCGCGTGGAGCTGTGTGTGGCGCGCGC	1204
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Db	1205	GGGCACTCCGAGGAGAGCTGCAGCTTCGAGAGGAGTGCCTGTGGCGCTTCGACTGGTGC	1264
Qy	1141	TGCGTAACTAGTSCAACCGCTGCCTGTGGCAGAGAGCTCAGGCTCTGCCTGTGACGC	1200
Db	1265	TGCGTAACTAGTSCAACCGCTGCCTGTGGCAGAGAGCTCAGGCTCTGCCTGTGACGC	1324
Qy	1201	CGCGCGCGCGCGCTAGCTGACTTCGCGCGAGCGGCTGGCTCGCAGCTGTGGAGCTCAGGG	1260
Db	1325	CGCGCGCGCGCGCTAGCTGACTTCGCGCGAGCGGCTGGCTCGCAGCTGTGGAGCTCAGGG	1384

1261	QY	CACGGGACGGGGGCGCTCTGGCGGTCTGAGGCCGACGCTCTCCCTGCGCAAGGCCCACTC	1320
1385	DB	CACGGGACCGGGGGGCTCTGGCGGTCTGAGGCCGACGCTCTCCCTGCGCAAGGCCCACTC	1444
1321	QY	CCAGGSGCTCTGGAAATGGTGGGCGAGGGGGCTTAGAGGAAACGGCCACCCACGAGGGGCC	1380
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1625	DB	AGGGCGTGGGTAATCTGGGCTCCCGACGAATGCTGGCCACAGGATGGTGGGTGAGGTTAGT	1684
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1685	DB	ATCAATAAGAGATATTAAACCA	1706

RESULT 8	1702 bp	DNA	linear	PAT 18-JUN-2001
E38394	E38394	Wt-6 polynucleotide and	Wt-6 polynucleotide.	
LOCUS				
DEFINITION				

E38394
 VERSION E38394.1 GI:13023195
 KEYWORDS JP 2000060575-A/1.
 SOURCE Hmo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 (Bases 1 to 1702)
AUTHORS
Michael, R.B. and Tania, I.T.
TITLE
Wnt-6 polypeptide and Wnt-6 polynucleotide
JOURNAL
Patent: JP 2000060575-A 1 29-FEB-2000;

COMMENT	OS Homo sapiens (human)	SMITHKLINE BEECHAM CORP PUBLIC LTD CO
	PN JP 2000060575-A/1	

PD	29-FEB-2000	
PF	29-JAN-1999	JP 1999022239
PR	12-AUG-1998	GB 9817586:2

PI MICHAEL R BANESU, TANIA TAMUSON TESTA
C12N15/09, A61K31/00, A61K31/00, A61K31/00, A61K38/00, A61K39/395,
PC A61K45/00

PC A61K48/00,
PC A61K48/00,C07K14/47,C07K16/18,C12N1/10,C12N1/15,C12N1/19, PC
C12N1/21,C12N5/10,
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	Year	Location/Qualifiers
PC	C1ZP217/02, G0LN33/33, G0LN33/33/11, C1Z124/V0/G0LN33, C0P0LN33/12	
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Location/Qualifiers
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Db	1025	GGCTTGTGCGCGCGTCCGCAAGCTCAAGCGCGCGGCGGACGCGCTCTCTACGGC	1084
Qy	961	GGCGATTGGCGCGACTTCTGGGCGCCCGAAACCGACGCAAGGCTTCCCGGCGACGGGGT	1020
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Qy	1021	GGGCGCTGCAATAGCAGCGCGCGGACCTCAGCGGCTCGAGCTGCTGTGCTGGCGCGCG	1080
Db	1145	CGGCGCTGCAATAGCAGCGCGCGGACCTCAGCGGCTCGAGCTGCTGTGCTGGCGCGCG	1204
Qy	1081	GGGCAACCGCAGAGAGGCTGCAGCTCGAAGAGAGTGCCTGTGGCGCTTCACTGGTGC	1140
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Qy	1141	TGGGTAGTACAGTGGCAACCGCTGGCGTGGCGCAGAGCTCAGGCTCTGGCTGTGAGCC	1200
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Qy	1201	GGCGCGCGCGCTAGACTGACCTTGGCGAGCGGTGGTGGCACTGTGGAGCTCAGGG	1260
Db	1325	GGCGCGCGCGCTAGACTGACCTTGGCGAGCGGTGGTGGCACTGTGGAGCTCAGGG	1384
Qy	1261	CAGCGCACCGCGCGCTCTCGCGCTCGAGCCCGAGCTCTCCCTGCCAAGCGCCACTC	1320
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Qy	1321	CGAGGGCTCTGGAAATGTGAGGGGAGGGGCTTGAGAGGACGCCACCGCACGAGGGCC	1380
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Qy	1441	CTCCCTCCCTTGGCTCTAGAGGAGAAACAGTTTTTAGACTTGGAAAAAGCAAGCTCTAA	1500
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Qy	1501	AGGCGCTCTGGATACTGGGCTCCCGAGACTGTGGCGCACAGATGGTGGGTGAGGTAGT	1560
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Qy	1561	ATCAATAAAGACATTAA	1578
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LOCUS	AY009401	1702 bp	mRNA
DEFINITION	Homo sapiens WNT6 precursor (WNT6)	mRNA, complete cds.	
ACCESSION	AY009401		
VERSION	AY009401.1	GI:11693043	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
REFERENCE	1	(bases 1 to 1702)	

Search completed: April 3, 2004, 11:14:11
Job time : 4080.45 secs

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D6		
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Qy		
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D6		
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Qy		
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Qy		
1625	AGGCTCTCGATACTGGGCTCCCGAGACTGCTGGCCACAGGATGGTGGGTGAGGTAGT	1684
D6		
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D6		

OM nucleic - nucleic search, using sw model

Run on: April 2, 2004, 21:47:00 ; Search time 396.83 Seconds
(without alignments)
16957.243 Million cell updates/sec

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Perfect score: 1584
Sequence: 1 ggcgtccgcgcgtccgact.....ataagatatattaaaccacc 1584

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: geneseqn1960s.*
2: geneseqn1990s.*
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4: geneseqn2001as.*
5: geneseqn2001bs.*
6: geneseqn2002s.*
7: geneseqn2003as.*
8: geneseqn2003bs.*
9: geneseqn2003cs.*
10: geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	1584	100.0	1584	AAF93866	Aaf93866 Human cDN
3	1577.2	99.6	1726	ABX75316	Abx75316 Human cDN
4	1577.2	99.6	1726	AAD52541	Aad52541 WNT-6 DNA
5	1577.2	99.6	1726	ABZ81813	Abz81813 Ligand WN
6	1573.2	99.3	1702	AAZ91783	Aaz91783 Human Wnt
7	1434.4	90.6	1754	ACC51101	Acc51101 Human Sol
8	1434.4	90.6	1754	ACC51102	Acc51102 Human Sol
9	1333.8	84.2	1855	ACC51108	Acc51108 Human Sol
10	848.2	53.5	959	ADD78265	Add78265 Human CGD
11	520	32.8	526	AAF94068	Aaf94068 Primer sp
12	512	32.3	512	ABS70488	Abs70488 Human bon
13	466.6	29.5	803	AAD16763	Aad16763 Human nov

14	466.6	29.5	803	9	ADC22055	Adc22055 Human cDN
15	322	20.3	342	7	AEB23692	Aeb23692 Human GEN
16	213.2	13.5	1202	4	AAD16767	Aad16767 Human nov
17	213.2	13.5	1202	9	ADC22059	Acc22059 Human cDN
18	213.2	13.5	1228	3	AAZ290451	Aaz290451 Wnt-4AF a
19	213.2	13.5	1515	7	ABX62938	Abx62938 Human act
20	213.2	13.5	1515	4	AAI58045	Aai58045 Human pol
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22	211.6	13.4	2049	2	AAZ34081	Aaz34081 Human PRO
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24	211.6	13.4	2049	4	AAZ45964	Aaz45964 Human DNA
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32	211.6	13.4	2049	7	ACA90282	Acca90282 Novel hum
33	211.6	13.4	2049	7	ACC9389	Accc9389 Human sec
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35	211.6	13.4	2049	7	ACA93822	Acca93822 Human sec
36	211.6	13.4	2049	7	ACD15215	Accd15215 Human sec
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ALIGNMENTS

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AC AAF29359;
XX
XX
DT 20-APR-2001 (first entry)
XX
DE Amyloid-beta protein agglutination regulating factor DNA SEQ ID 5.
XX
KW Human; amyloid-beta protein; agglutination regulatory factor;
KW Alzheimer's disease; ds.
XX
OS Homo sapiens.
XX
XX WO200104259-A1.
XX
PD 18-JAN-2001.
XX
PF 06-JUL-2000; 2000WO-JP004515.
XX
XX
PR 08-JUL-1999; 99JP-00194179.
PR 18-OCT-1999; 99US-0159566P.
XX
PA (HELI-) HELIX RES INST.
XX

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DB		
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QY		
DB		
1561	ATCAATAAAGATATTAAACCACC	1584
QY		
DB		
1561	ATCAATAAAGATATTAAACCACC	1594
QY		
DB		

RESULT 2
AAF93866
ID AAF93866 standard: cDNA; 1584 BP.

XX	AAF93866;	(first entry)
AC		
XX		
DT	23-MAY-2001	

Human cDNA encoding a membrane or secretory protein: clone PSEC0220.

xx Human; secretory protein; membrane protein; vaccine; gene therapy;
kw
kw rheumatoid arthritis; diabetes; ss.
xx

How can we

	C
	A
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XX

XX

11-JAN-2000;

PK 02-1941-2000,
YY

PA (HELI-) HELIX RES INST.

PI Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama I, Hayashi N,

DR WPI; 2001-093989/11.

XX

PT gene therapy or as candidate target molecules in drug development.

PS Claim 1: SEQ ID NO 245: 609bp + Sequence Listing: English.

This invention relates to nucleic acid sequences AAF93744 - AAF93916 which encode human secretory or membrane proteins represented by AAF88317 - AAF88419. Included in the invention are primers AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the invention. The invention also includes methods for the production of antibodies directed against the proteins, and cDNA sequences, which can be used in vaccines. The polynucleotide sequences can be used in gene therapy. The polynucleotide sequences and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate secretory protein/membrane protein expression. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples. They may also be used to study the expression and function of secretory proteins/membrane polypeptides and their role in metabolism. The polypeptides may be used as antigens in the production of antibodies against them and in assays to identify modulators (agonists/antagonists).

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Db 781 TGGGATCATGGCGCTGGCACTGTGGCAGAGCTGCTCCATTTCCGAGGTGGGC 840

Qy 841 GCGGGCTGTGGAGCGTTTCCAGGGGGCTCAGCGGTGATGGGACCAACAGCGCAAG 900

Db 841 GCGGGCTGTGGAGCGTTTCCAGGGGGCTCAGCGGTGATGGGACCAACAGCGCAAG 900

Qy 901 GCGGTGTGGCGCGTCCGACGCTCAAGGGCGGGCGAGCGGACCTGCTCTAGGCG 960

Db 901 GCGGTGTGGCGCGTCCGACGCTCAAGGGCGGGCGAGCGGACCTGCTCTAGGCG 960

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Db 1081 GGGCACCGGACGAGAGCGTGCAGCTGGAAGAGAACTGCTGTGGCGTTCACACTGGTGC 1140

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Db 1261 CACGGCTACCGCGCGCTGCGCGCTGGAGCGGCTGCTCCCTGGCAAGGCCCACTC 1320

Qy 1321 CCAAGGCTCTGGAATGCTGAGGCGAGGGCTTGAGAGGAAAGCGCCACCAAGAGGCC 1380

Db 1321 CCAAGGCTCTGGAATGCTGAGGCGAGGGCTTGAGAGGAAAGCGCCACCAAGAGGCC 1380

Qy 1381 AGGGCGCAGAGCGCCCGGAAAGGGCTGGGGAGCGTTTAAAGGACCTGTACAGGCG 1440

Db 1381 AGGGCGCAGAGCGCCCGGAAAGGGCTGGGGAGCGTTTAAAGGACCTGTACAGGCG 1440

Qy 1441 CTCCTCCCTTGGCTCTAGGAGGAAACAGTTTTTAGACTGGAAAAAGCCAGTCTAA 1500

Db 1441 CTCCTCCCTTGGCTCTAGGAGGAAACAGTTTTTAGACTGGAAAAAGCCAGTCTAA 1500

Qy 1501 AGGCTCTGGATCTGGGCTCCGACGACCTGCTGGCCACAGGATGGTGGGTAGGTAGT 1560

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Qy 1561 ATCAATAAAGATATTTAAACACC 1584

Db 1561 ATCAATAAAGATATTTAAACACC 1584

RESULT 3
 ABX75316
 ID ABX75316 standard; cDNA; 1726 BP.
 XX

AC ABX75316;
 XX 25-MAR-2003 (first entry)
 DT Human cDNA encoding WNT-6.
 XX
 DE Gene; Notch; Wnt; embryonic stem cell; embryogenesis; as;
 XX differentiation; ligand; Parkinson's disease; Huntington's disease;
 KW motor neuron disease; heart disease; diabetes; liver disease; human;
 KW cirrhosis; renal disease; AIDS; acquired immunodeficiency syndrome.
 XX
 OS Homo sapiens.
 XX
 XX W020027204-A2.
 XX 03-OCT-2002.
 XX 25-MAR-2002; 2002WO-GS01195.
 XX 23-MAR-2001; 2001GB-00007296.
 XX 23-MAR-2001; 2001GB-00007299.
 XX 17-APR-2001; 2001GB-00009346.
 XX (AXOR-) AXORDIA LTD.
 XX Andrews P, Walsh J, Gokhale P;
 P: WPI; 2003-092852/08.
 DR P-PSDB; AEU55888.
 XX
 XX Modulating the differentiation of embryonic stem cells by providing
 PT ligands which bind receptors in the Notch and Wnt pathways, useful for
 PT treating diseases such as Parkinson's, Huntington's, heart disease,
 PT diabetes and AIDS.

Claim 3; Fig 42; 121bp; English.

The invention relates to modulating the differentiation of an embryonic stem cell, comprising: (a) providing a culture of embryonic stem cells; (b) providing at least one ligand or its active binding fragment, capable of binding its cognate receptor polypeptide expressed by the embryonic stem cell; (c) forming a culture comprising embryonic stem cells and the ligand; and (d) growing the cell culture. Also included are: (1) Modulating the differentiation of embryonic stem cells, comprising: (a) providing a cell transfected with a nucleic acid molecule selected from: (i) any of 9 fully defined Wnt nucleic acid sequences; (ii) a nucleic acid molecule that hybridizes to the nucleic acid in (i), and which encodes a ligand capable of modulating embryonic stem cell differentiation, or capable of binding a Wnt receptor; or (iii) nucleic acid molecules which are degenerate as a result of the genetic code to the sequences of (i) or (ii); (b) forming a culture comprising the cell identified in (a) with an embryonic stem cell; and (c) growing the culture for the maintenance and/or differentiation of the embryonic stem cell; (2) Inhibiting the differentiation of embryonic stem cells, comprising: (a) providing at least one polypeptide or its active fragment, that are inhibitors of the Wnt signalling pathway; (b) forming a culture comprising the cell identified in (a) with an embryonic stem cell; and (c) growing the culture for the maintenance of embryonic stem cells in an undifferentiated state; or (3) Inhibiting the differentiation of embryonic stem cells, comprising: (a) providing a cell transfected with a nucleic acid molecule selected from: (i) a molecule encoding a Wnt inhibitory polypeptide; (ii) a molecule which hybridizes to the molecule of (i) and encodes a polypeptide capable of inhibiting Wnt signalling;

CC and (iii) nucleic acid molecules which are degenerate as a result of the
CC genetic code to the sequences of (i) or (ii); (b) forming a culture
CC comprising the cell identified in (a) with an embryonic stem cell; and
CC (c) growing the culture for the maintenance of embryonic stem cells in an
CC undifferentiated state; and (4) A cell, therapeutic cell or cell culture
CC obtainable by any of the methods cited above. The therapeutic cell of the
CC present invention is useful in the treatment of an animal, preferably a
CC human, comprising administering a cell composition comprising embryonic
CC stem cells which have been induced to differentiate into at least one
CC cell-type. The cell is also useful for the manufacture of a composition
CC for use in treatment of diseases such as Parkinson's disease,
CC Huntington's disease, motor neuron disease, heart disease, diabetes,
CC liver disease (e.g. cirrhosis), renal disease and AIDS (acquired
CC immunodeficiency syndrome). The present sequence encodes a Wnt or
XX Notch pathway protein (i.e. a ligand for the method of the invention)
SQ Sequence 1726 BP; 274 A; 631 C; 570 G; 251 T; 0 U; 0 Other;

Query Match 99.6%; Score 1577.2; DB 7; Length 1726;
Best Local Similarity 99.8%; Pred. No. 3.9e-276;
Matches 1579; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GGCCTCGGGGCGCTGCACTGAGAGCCGGGGCCCTCGGGGCGCGGGTTCCGCCCGCAGCC 60
DB 125 GGCCTCGGGGCGCTGCGACTGAGAGCCGGGGCCCTCGGGGCGCGGGTTCCGCCCGCAGCC 184
QY 61 TCGCCCTCCCTGCCACCCGGGGCGCGGTAGGGCGGTACAGATGCTGCCGGCCCTTACCCCTCC 120
DB 185 TCGCCCTCCCTGCCACCCGGGGCGCGGTAGGGCGGTACAGATGCTGCCGGCCCTTACCCCTCC 244
QY 121 CGGCTCGGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 150
DB 245 CGGCTCGGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 304
QY 181 GCTGTGGGCGACCCCTTGCTATGAGCCCTACAGCATCTGACAGAGGCACTGGGGGCTG 240
DB 305 GCTGTGGGCGACCCCTTGCTATGAGCCCTACAGCATCTGACAGAGGCACTGGGGGCTG 364
QY 241 GCGGGGCGGCGAGCGGAGTGTGTGCGAGGCTGAGCGGAGAGTGTGTGTGTGTGTGTGTGTGT 300
DB 365 GCGGGGCGGCGAGCGGAGTGTGTGCGAGGCTGAGCGGAGAGTGTGTGTGTGTGTGTGTGTGT 424
QY 301 GGGGCGCGGCTCGGGGTGCGAGAGTGCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTC 360
DB 425 GGGGCGCGGCTCGGGGTGCGAGAGTGCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTC 484
QY 361 TCCAGCCACAGAGGCGCTTTGAGCGCATCTGCAACAGAGCATTTGGGAGAGCGGCGCTTC 420
DB 485 TCCAGCCACAGAGGCGCTTTGAGCGCATCTGCAACAGAGCATTTGGGAGAGCGGCGCTTC 544
QY 421 GTGTTCGCGCATCATCTGCGGGCGGGCGGCGAGCCAGCCGCTGTCAGCGAGGCTGTCTATGGGC 480
DB 545 GTGTTCGCGCATCATCTGCGGGCGGGCGGCGAGCCAGCCGCTGTCAGCGAGGCTGTCTATGGGC 604
QY 481 GAGCT 540
DB 605 GAGCT 664
QY 541 CTGCCCGGCGACCCCGGAGCCCTTGGGCGCGCGGGGCTCCCGCGGAGGAGCGGCGCGCTGG 600
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DB 965 GCGGGCTGCTGGAGGCTTCCACGGGGCTCAGCGGTGATGGGCAACCAACGAGGGCAAG 1024
QY 901 GCGCTGCTGCGCGGCTGCGGAGCTCAAGCGCGCGGGCGGAGGAGCTGCTAGGCG 960
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QY 1141 TCGGTAGTACAGTGGCAACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
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DB 1625 AGGGCTCTGGATGCTGGGCTGCGGAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1684

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Qy	1441	CTCCCTCCCTTGGCTCTAGGAGGAACAGTTTTTTAGACTGGAAAAAGCCAGTCTAA	1500
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XX	01-JUN-2000 (first entry)		
XX	Humar Wnt-6 protein coding sequence.		
DE	Human; Wnt-6 protein; Wnt-6-related disease; schizophrenia; epilepsy;		
KW	bipolar disorder; unipolar disorder; Alzheimer's disease; cancer;		
KW	squamous cell carcinoma; cardiovascular disease; stroke; diagnosis;		
KW	developmental disorder; lamellar ichthyosis; therapy; ss.		
XX	Homo sapiens.		
XX	EP979870-Al.		
PN	16-FEB-2000.		
PD	27-OCT-1998; 98EP-00203616.		
PF	12-AUG-1998; 98CB-00017586.		
PR	(SMK) SMITHKLINE BEECHAM PLC.		
XX	PA		
XX	XX		

RESULT 6

AAZ91783

2D AAZ91783 standard; DNA; 1702 BP.

AC AAZ91783;

XX

DT 01-JUN-2000 (first entry)

XX

DE Human Wnt-6 protein coding sequence.

[illegible]

KW Human; Wnt-6 protein; Wnt-6-related disease; schizophrenia; epilepsy;

KW bipolar disorder; unipolar disorder; Alzheimer's disease; cancer;

RW squamous cell carcinoma; cardiovascular disease; stroke; diagnosis;

RW developmental disorder; lamellar ichthyosis; therapy; ss.
VV

20 Home care, one
 21
 22

XX
02 ному сартену.
02

PN E9979870-A1-

[illegible]

PD 16-FEB-2000.

XX


PF 27-OCT-1998; 98EP-00203616.

XX

PR 12-AUG-1998; 98GB-00017586.

XX

PA (SMIK) SMITHKLINE BEECHAM PLC.



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Job time : 404.83 secs

GenCore version 5.1.6
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QM nucleic - nucleic search, using sw model

Run on: April 3, 2004, 11:14:53 ; Search time 380.642 Seconds
(without alignments)
15564.412 Million cell updates/sec

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Perfect score: 1584
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2466186 seqs, 1870095128 residues

Total number of hits satisfying chosen parameters: 4932372

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Published Applications NA:*

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- 18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			DB ID	Description
	Score	Match	Length		
1	1577.2	99.6	1726	14 US-10-285-976-18	Sequence 18, Appl
2	1434.4	90.6	1754	10 US-09-992-600A-83	Sequence 83, Appl
3	1434.4	90.6	1754	10 US-09-992-600A-85	Sequence 85, Appl
4	1434.4	90.6	1754	10 US-09-924-340-83	Sequence 83, Appl
5	1434.4	90.6	1754	10 US-09-924-340-85	Sequence 85, Appl

6	134.4	90.6	1754	10	US-09-992-095B-83	Sequence 83, Appl
7	134.4	90.6	1754	10	US-09-992-095B-85	Sequence 85, Appl
8	134.4	90.6	1754	10	US-09-959-570-83	Sequence 83, Appl
9	134.4	90.6	1754	10	US-09-959-570-85	Sequence 85, Appl
10	134.4	90.6	1754	14	US-10-000-483-83	Sequence 83, Appl
11	134.4	90.6	1754	14	US-10-000-483-85	Sequence 85, Appl
12	134.4	90.6	1754	14	US-10-000-986-83	Sequence 83, Appl
13	134.4	90.6	1754	14	US-10-000-986-85	Sequence 85, Appl
14	134.4	90.6	1754	14	US-10-154-678-83	Sequence 83, Appl
15	134.4	90.6	1754	14	US-10-154-678-85	Sequence 85, Appl
16	134.4	90.6	1754	14	US-10-001-142-83	Sequence 83, Appl
17	134.4	90.6	1754	14	US-10-001-142-85	Sequence 85, Appl
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25	133.8	84.2	1855	14	US-10-001-142-97	Sequence 97, Appl
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28	347.4	21.9	499	9	US-09-833-381-206	Sequence 206, Appl
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30	213.2	13.5	1198	14	US-10-285-976-12	Sequence 12, Appl
31	213.2	13.5	1202	9	US-09-764-903-28	Sequence 28, Appl
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33	213.2	13.5	1515	13	US-10-002-600-54	Sequence 54, Appl
34	213.2	13.5	1598	13	US-10-038-841-251	Sequence 251, App
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ALIGNMENTS

RESULT 1
US-10-285-976-18
Sequence 18, Application US/10285976
Publication No. US20030165500A1
GENERAL INFORMATION:
APPLICANT: Rhee, Chae-Seo
APPLICANT: Malini, Sen
APPLICANT: Wu, Christina
APPLICANT: Leoni, Lorenzo M.
APPLICANT: Cort, Maripat
APPLICANT: Carson, Dennis A.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Wnt and Frizzled Receptors as Targets for Immunotherapy
FILE OF INVENTION: In Head and Neck Squamous Cell Carcinomas
FILE REFERENCE: 023070-1303200S
CURRENT APPLICATION NUMBER: US/10/285,976
CURRENT FILING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: US 60/287,995

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Qy 1561 ATCAATAAGATATTTAAACCA 1582

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- EST: +
- 1: em_estba:*
 - 2: em_esthum:*
 - 3: em_estin:*
 - 4: em_estma:*
 - 5: em_estov:*
 - 6: em_estpl:*
 - 7: em_estro:*
 - 8: em_hic:*
 - 9: gb_est1:*
 - 10: gb_est2:*
 - 11: gb_rtc:*
 - 12: gb_est3:*
 - 13: gb_est4:*
 - 14: gb_est5:*
 - 15: em_estfun:*
 - 16: em_estom:*
 - 17: em_gss_hum:*
 - 18: em_gss_inv:*
 - 19: em_gss_pln:*
 - 20: em_gss_vrt:*
 - 21: em_gss_fun:*
 - 22: em_gss_man:*
 - 23: em_gss_mus:*
 - 24: em_gss_pro:*
 - 25: em_gss_rod:*
 - 26: em_gss_phg:*
 - 27: em_gss_vrl:*
 - 28: gb_gss1:*
 - 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
c 1	695.2	43.9	1030	10	BF568920	BF568920 602184074
c 2	683	43.1	1018	29	AY404151	AY404151 Homo sapi
c 3	676.4	42.7	1033	10	BF568080	BF568080 602184074
c 4	642.6	40.6	947	10	BE410061	BE410061 601300578
c 5	626.6	39.6	738	10	BF058854	BF058854 7K35e06.x
c 6	589	37.2	661	10	BE744521	BE744521 601577308
c 7	566.2	35.7	1018	29	AY404153	AY404153 Mus muscu
c 8	563.4	35.6	580	12	BM763339	BM763339 K-EST0044
c 9	548.2	34.6	730	10	BE382983	BE382983 601296875
c 10	540	34.1	918	12	BI107139	BI107139 602894567
c 11	532.2	33.6	998	29	AY404152	AY404152 Pan trogl
c 12	530.4	33.5	587	10	AW872887	AW872887 hg70b10.x
c 13	527.2	33.3	595	10	BE392594	BE392594 601307417
c 14	513.4	32.4	565	10	BF057511	BF057511 7K45b06.x
c 15	512.6	32.4	912	13	EU514438	EU514438 AGENCOURC
c 16	510	32.2	524	13	EX100389	EX100389 EX100389
c 17	495.2	31.5	521	12	BM687468	BM687468 UT-E-CRO-
c 18	491.8	31.0	918	12	BI106115	BI106115 602891163
c 19	491	31.0	491	10	BE645584	BE645584 7672f03.x
c 20	490	30.9	505	12	BM849242	BM849242 X-EST0129
c 21	479	30.2	479	9	AI123434	AI123434 qa98c09.x
c 22	473	30.0	476	9	AI127113	AI127113 qb86a10.x
c 23	470.8	29.7	475	9	AI400680	AI400680 tg89h04.x
c 24	468.2	29.6	524	9	AI191771	AI191771 qd62f02.x
c 25	467.4	29.5	469	10	AW166343	AW166343 xn51q07.x
c 26	461	29.1	462	9	AI246658	AI246658 qi27b10.x
c 27	461	29.1	790	9	AI436419	AI436419 ti01b04.x
c 28	459	29.0	460	10	BF439281	BF439281 n8b62c09.x
c 29	457.4	28.9	459	9	AI126905	AI126905 qb95e12.x
c 30	455.6	28.8	599	9	AI599019	AI599019 EST250722
c 31	439.4	27.7	442	9	AI126936	AI126936 qb95h12.x
c 32	436.8	27.6	513	9	AA482530	AA482530 zv05f03.f
c 33	430.4	27.2	459	9	AA235929	AA235929 zs43e08.f
c 34	430	27.1	430	9	AI378801	AI378801 tc67c08.x
c 35	429.2	27.1	535	9	AI600244	AI600244 EST251947
c 36	426	26.9	426	9	AI333576	AI333576 qq06f12.x
c 37	426	26.9	427	10	BF111582	BF111582 7129q07.x
c 38	425.6	26.9	485	9	AA236986	AA236986 zs43e07.s
c 39	425.4	26.9	521	14	CD673352	CD673352 fg23h08.y
c 40	424.4	26.8	427	12	BM720290	BM720290 UT-E-EJO-
c 41	422.2	26.7	479	9	AI207825	AI207825 ao89g04.x
c 42	415.8	26.2	572	14	CB615347	CB615347 AMGNNUCIN
c 43	410.6	25.9	632	10	BF033777	BF033777 601454120
c 44	401.6	25.4	916	10	BF163843	BF163843 601772354
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Search completed: April 3, 2004, 16:37:25
Job time : 2685.05 secs

OM nucleic - nucleic search, using sw model

Run on: April 3, 2004, 00:09:01 ; Search time 4071.25 Seconds
(without alignments)
16863.461 Million cell updates/sec

Title: US-10-030-269A-5
Perfect score: 1584
Sequence: 1 gcgtctgcgcgcgcgcgcact.....ataagatatttaaacacc 1584

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: gb.ba.*
- 2: gb.hg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
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- 41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1584	100.0	1584	9	AK075522 Homo sapi
5	1577.2	99.6	1726	6	AX565675 Sequence
6	1577.2	99.6	1726	6	AX597075 Sequence
7	1577.2	99.6	1726	6	AX701352 Sequence
8	1573.2	99.3	1702	6	E38394 Wnt-6 polyp
9	1573.2	99.3	1702	9	AY089401 Homo sapi
10	1482.8	93.6	1506	9	BC004329 Homo sapi
11	1447.2	91.4	1452	9	AB059570 Homo sapi
12	1434.4	90.6	1754	6	AX616399 Sequence
13	1434.4	90.6	1754	6	AX616401 Sequence
14	1333.8	84.2	1855	6	AX616413 Sequence
15	1092.8	69.0	1098	12	BT009885 Synthetic
16	1091.2	68.9	1098	9	BT007456 Homo sapi
17	93.4	57.7	1669	10	BC048700 Mus muscu
18	869.4	54.9	1435	10	M89900 Mouse Wnt-6
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24	512	32.3	512	6	AF222094 Sequence
25	415.6	26.2	205178	2	AC132020 Rattus no
26	415.6	26.2	228187	2	AC127107 Rattus no
27	415.6	26.2	287955	2	AC095777 Rattus no
28	403.6	23.3	227724	2	AF336381 Mus muscu
29	322	20.3	342	6	AX586690 Sequence
30	319.4	20.2	339	6	AR412407 Sequence
31	319.4	20.2	339	6	BD107960 EST and e
32	237.8	15.0	304078	2	AC129703 Rattus no
33	237.2	15.0	2298	3	AB044713 Gryllus b
34	230.4	14.5	2656	3	AF361015 Branchios
35	213.2	13.5	1182	9	AF316543 Homo sapi
36	213.2	13.5	1344	9	BC057781 Homo sapi
37	212.2	13.4	353	5	AF378331 Gallus ga
38	211.6	13.4	2049	9	AX376012 Sequence
39	211.6	13.4	2049	9	AX358947 Homo sapi
40	209	13.2	2368	6	AX578080 Sequence
41	208.2	13.1	1061	9	AB061675 Homo sapi
42	205	12.9	1056	6	AF122699 Sequence
43	205	12.9	1056	6	E31445 Novel compo
44	205	12.9	1056	6	AX006320 Sequence
45	205	12.9	1056	6	AX565671 Sequence

ALIGNMENTS

RESULT 1
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LOCUS AX136323 1584 bp DNA linear PAT 30-MAY-2001
DEFINITION Sequence 245 from Patent EP1067182.
ACCESSION AX136323
VERSION AX136323.1 GI:14272729

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Hemo.

REFERENCE 1
Ota, T., Isogai, T., Nishikawa, T., Kawai, Y., Sugiyama, T. and

Hayashi, K.
Secretory protein or membrane protein
Patent: EP 1067182-A 245 1C-JAN-2001;
Helix Research Institute (JP)

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RECKCHGLSGSCALRTQWKLPPFRFVNGARLLERFGASVMTGNDGKALLPAVETL
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CDS

ORIGIN

Query Match 100.0%; Score 1584; DB 6; Length 1584;
Best Local Similarity 100.0%; Pred. No. 1.1e-213;
Matches 1584; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1561 ATCAATAAAGATATTTAAACACC 1584

RESULT 3
BD123614
LOCUS
DEFINITION
SECRETORY protein or membrane protein.
ACCESSION
BD123614.1 GI:23218559
VERSION
BD123614.1
KEYWORDS
JP 2002017376-A/123.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1584)
AUTHORS Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.
TITLE Secretory protein or membrane protein
JOURNAL Patent: JP 2002017376-A 123 22-JAN-2002;
HELIIX RESEARCH INSTITUTE
COMMENT OS Homo sapiens (human)
PN JP 2002017376-A/123
PD 22-JAN-2002
PF 07-JUL-2000 JP 2000253173
PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,YURI KAWAI,TOMOYASU
PI SUGIYAMA,
PI KOJI HAYASHI
PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/21,C12N5/10, C12N5/10, C12P21/02,C12Q1/68//C12P21/08,C12N15/00,C12N5/00 CC
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Best Local Similarity 100.0%; Pred. No. 1.1e-213;
Matches 1584; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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VERSION AX565675.1 GI:2600994

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 Andrews, P., Walsh, J. and Gokhale, P.

AUTHORS

TITLE

Stem cell

JOURNAL

Patent: WO 02077204-A 36 03-OCT-2002;

FEATURES

Location/Qualifiers

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ORIGIN

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Matches 1579; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 1565 CTCGCTCCGCTTGGGCTCTAGAGGAAACAGTTTTTTAGACTGGAAAAAGCCAGTCTAA 1624
QY 1501 AGGCTCTGATGACTGGGCTCCGCAAGTCTGGGCAAGATGCTGGGTGAGGTAGT 1560
Db 1625 AGGCTCTGATGACTGGGCTCCGCAAGTCTGGGCAAGATGCTGGGTGAGGTAGT 1684
QY 1561 ATCAATAAAGATATTTAAACCA 1582
Db 1685 ATCAATAAAGATATTTAAACCA 1706

RESULT 7
AX701352
LOCUS AX701352 1726 bp DNA linear PAT 03-APR-2003
DEFINITION Sequence 21 from Patent WO03012082.
ACCESSION AX701352
VERSION AX701352.1 GI:29537001
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Andrews, P., Walsh, J., and Gokhale, P.
TITLE Method for modulating stem cell differentiation using stem loop rna
JOURNAL Patent: WO 03012082-A 21 13-FEB-2003;
Aordia Limited (GB)
FEATURES
source 1..1726
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 99.6%; Score 1577.2; DB 6; Length 1726;
Best Local Similarity 99.8%; Pred. No. 1e-212;
Matches 1579; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCCTCGCGGCTCGACTGAGCGCGGGGCTCGCGCGCGGTTGCGCGCGGCC 60
Db 125 GCCTCGCGGCTCGACTGAGCGCGGGGCTCGCGCGCGGTTGCGCGCGGCC 184
QY 61 TCGCCGCTGCGCCACCGCGCGCGGCTAGGCGGTCAGATGCTGCCGCGCTTACCTCC 120
Db 185 TCGCCGCTGCGCCACCGCGCGCGGCTAGGCGGTCAGATGCTGCCGCGCTTACCTCC 244
QY 121 CGCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db 245 CGCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 304
QY 181 GCTGTGGCAGCGGCTTGTATGAGCGCTTACAGATCTGCAAGAGGCAAGCGCGCTG 240
Db 305 GCTGTGGCAGCGGCTTGTATGAGCGCTTACAGATCTGCAAGAGGCAAGCGCGCTG 364
QY 241 GCGGCGCGGCAAGCGGCTTGTGCGAGGCTAGCGCGGAGTGGTGGCAGAGTACTGG 300
Db 365 GCGGCGCGGCAAGCGGCTTGTGCGAGGCTAGCGCGGAGTGGTGGCAGAGTACTGG 424
QY 301 GCGGCGCGGCTCGGAGGCTGCGAGAGTGCAGATTCCGCTTCGCGCGCTGGAATTGC 360

Db 425 GGCGCGCGGCTCGGGGTGCGAGAGTGCACAGTTCAGTTCGGCTTCGCGCGCTGGAATTGC 484
QY 361 TCCACACACAGCAAGCGCTTTGGAGCGCATCCTGCAACAGAGCATTCGGGAGAGCGGCTTC 420
Db 485 TCCACACACAGCAAGCGCTTTGGAGCGCATCCTGCAACAGAGCATTCGGGAGAGCGGCTTC 544
QY 421 GTGTTGGGCACTCTGCGGCGCGCGCGCAAGCGCGCTGCAAGAGGCTGTTCTATGGGC 480
Db 545 GTGTTGGGCACTCTGCGGCGCGCGCGCAAGCGCGCTGCAAGAGGCTGTTCTATGGGC 604
QY 481 GAGCTGCTGCAATGCGGCTGCCAGCGCGCGCTGGGCGCGCTGCCGCGCTCGGCG 540
Db 605 GAGCTGCTGCAATGCGGCTGCCAGCGCGCGCTGGGCGCGCTGCCGCGCTCGGCG 664
QY 541 CTGCCGCGCAAGCGCGCGCGCGCTGCCGCGCGCTGGGCGCGCTGCCGCGCGCTCGG 600
Db 665 CTGCCGCGCAAGCGCGCGCGCGCTGCCGCGCGCTGGGCGCGCTGCCGCGCGCTCGG 724
QY 601 GAGTGGGAGGCTGCGGCGCGAGAGCTGAGCTTGGGAGAGGAGAGTCTTTATG 560
Db 725 GAGTGGGAGGCTGCGGCGCGAGAGCTGAGCTTGGGAGAGGAGAGTCTTTATG 784
QY 661 GACGCGCGCACAAGCGGCGCGAGAGATCCGCGCGTTGGTCAACTGCAACAAC 720
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QY 721 GAGGCGGAGGCTGCGGCGCGAGAGCAAGCGCGCGCTGCAAAATGCCAGCGGCTG 780
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QY 781 TCGGAGATCATGCGGCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCG 840
Db 905 TCGGAGATCATGCGGCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCG 964
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QY 901 GCGTGTGCGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCG 960
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Db 1085 GCGGATTCGCGCGCTTCTGCGGCGCGCGCTGCGGCGCGCTGCGGCGCGCTGCGGCGCG 1144
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Db 1265 TCGTGTAGTACAGTGCACCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCG 1324
QY 1201 GCGGCGCGGCGCTGAGTGTGCTTGGCGAGCGGCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCG 1260
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DB		
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QY		
1445	CA GGG CTT CTG AAA T TGT GAG CGC GAG GGG CTT GAG A GAA CGC CCA CCA CCG A GAA GGC CC	1504
DB		
1361	AGG GCG CCA GAG CGC CCG AAA GCG GCT CGG GAG GCG TTT AAA GGA CAC GTT CAC AG GC CC	1440
QY		
1505	AGG GCG CCA GAG CGC CCG AAA GCG GCT CGG GAG GCG TTT AAA GGA CAC GTT CAC AG GC CC	1564
DB		
1441	CT CCG CTT CCG CTT GGC CTT CT AGG AGG AACA CAG TTT TTT AGA CTT GAAAA AAG CCA CTT CAA	1500
QY		
1565	CT CCG CTT CCG CTT GGC CTT CT AGG AGG AACA CAG TTT TTT AGA CTT GAAAA AAG CCA CTT CAA	1624
DB		
1501	AGG CCG TTT GAT ACT GGG CTT CCG AAG ACT GCT GCG CAC AGA GAT GGT GCG TGA GTT TAT	1560
QY		
1625	AGG CCG TTT GAT ACT GGG CTT CCG AAG ACT GCT GCG CAC AGA GAT GGT GCG TGA GTT TAT	1684
DB		
1561	ATCA ATA AGA TAT TTA	1578
QY		
1685	ATCA ATA AGA TAT TTA	1702
DB		

Search completed: April 3, 2004, 11:24:11
Job time : 4080.45 secs

OM nucleic - nucleic search, using sw model

Run on: April 2, 2004, 21:47:00 ; Search time 396.83 Seconds
(without alignments)
16957.243 Million cell updates/sec

Title: US-10-030-269A-5
Perfect score: 1584
Sequence: 1 gcgcgcgcgcgcgcgcact.....ataagatatttaaccacc 1584

Scoring table: IDENTITY_NUC
Gapop 10.0 ; Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues
Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: geneseqn1990as:*
3: geneseqn2000as:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004as:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1584	100.0	1584	4	Aaf29359 Anyloid-b
2	1584	100.0	1584	5	Aaf93866 Human cDN
3	1577.2	99.6	1726	7	Abx75316 Human cDN
4	1577.2	99.6	1726	7	Aad52541 WNT-6 DNA
5	1577.2	99.6	1726	7	Abz81813 Ligand WN
6	1573.2	99.3	1702	3	Aaz91783 Human wnt
7	1434.4	90.6	1754	7	Acc51101 Human Sol
8	1434.4	90.6	1754	7	Acc51102 Human Sol
9	1333.8	84.2	1855	7	Acc51108 Human Sol
10	848.2	53.5	959	9	AdD78265 Human CGD
11	520	32.8	526	5	Aaf94068 Primer sp
12	512	32.3	512	6	AbS70488 Human bon
13	466.6	29.5	803	4	Aad16763 Human nov

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16	213.2	13.5	1202	4	AAD16767	Aad16767 Human nov
17	213.2	13.5	1202	9	ADC22059	Adc22059 Human cDN
18	213.2	13.5	1228	3	AAZ90451	Aaz90451 Wnt-4AF a
19	213.2	13.5	1515	7	ABX62938	Abx62938 Human act
20	213.2	13.5	1598	4	AAI58045	Aai58045 Human pol
21	211.6	13.4	1598	4	AAI59831	Aai59831 Human pol
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24	211.6	13.4	2049	4	AAZ45964	Aaz45964 Human DNA
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28	211.6	13.4	2049	7	ACC87547	Acc87547 Human sec
29	211.6	13.4	2049	7	ACC86933	Acc86933 Human sec
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42	211.6	13.4	2049	7	ACD02982	Act02982 Novel hum
43	211.6	13.4	2049	7	ACD01797	Act01797 Novel hum
44	211.6	13.4	2049	7	ACA91989	Act91989 Novel hum
45	211.6	13.4	2049	7	ACA63649	Act63649 Novel hum

ALIGNMENTS

RESULT 1

AAF29359	ID	AAF29359	standard; DNA; 1584 BP.
XX	XX	AAF29359;	
XX	AC	AAF29359;	
XX	XX	20-APR-2001 (first entry)	
XX	DE	Anyloid-beta protein agglutination regulating factor DNA SEQ ID 5.	
XX	DE	Human; amyloid-beta protein; agglutination regulatory factor:	
XX	KW	Human; amyloid-beta protein; agglutination regulatory factor:	
XX	KW	Alzheimer's disease; ds.	
XX	XX	Homo sapiens.	
XX	OS	Wo200104299-A1.	
XX	PN	18-JAN-2001.	
XX	PD	06-JUL-2000; 2000WO-JP004515.	
XX	PF	08-JUL-1999; 99JP-00194179.	
XX	PR	18-OCT-1999; 99US-0159586P.	
XX	XX	(HELI-) HELIX RES INST.	

PI Ota T, Isogai T, Nishikawa T, Kawai Y, Yamazaki M, Satoh S;
PI Akakawa H, Morita M;
DR WPI: 2001-138347/14.
DR P-FSDB; AAB49769.
XX
PT Polynucleotide encoding Amyloid-beta protein agglutination-controlling
PT factor, useful for inhibiting or promoting agglutination or sedimentation
PT of amyloid-beta protein and in diagnosis and screening drugs for
PT Alzheimer's disease.
XX
PS Claim 1: Page 49-51; 72pp; Japanese.
XX
CC This invention relates to polynucleotides AAF29357 - AAF29361 which
CC encode proteins AAB49767 - AAB49771. The proteins inhibit or promote the
CC agglutination of amyloid beta protein. The protein and polynucleotide
CC sequences are useful in the diagnosis of Alzheimer's disease. They are
CC also useful for screening drugs which are useful for treating Alzheimer's
CC disease
XX
SQ Sequence 1584 BP; 245 A; 572 C; 531 G; 236 T; 0 U; 0 Other;
Query Match 100.0%; Score 1584; DB 4; Length 1584;
Best Local Similarity 100.0%; Pred. No. 2.3e-277;
Matches 1584; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Y 1 GGGCTGGCGGCTCGCACTGAAGCCCGGGCCCTCGCGCGCGCGGTTCGCCCGCGAGCC 60
D 1 GCGCTCGCGCGGCTCGCACTGAAGCCCGGGGCGCTCGCGCGCGCGGTTCGCCCGCGAGCC 60
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D 301 GCGGCGCGCGCTCGGGGTGCGAGAGTGCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTCAG 360
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D 361 TCCAGCCACAGCAAGGCTTTGGAGCATCTGACATCTGACATCTGACATCTGACATCTGACATCTGAC 420
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DB 541 CTGCGCGCGCACCCCGCGAGCCCTGCGCGCGCGCGAGCGCGAGCGCGAGCGCGAGCGCGAGCG 600
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DB 601 GAGTGGGAGGCTCGCGCGAGCGAGCTTCGCGGAGCGAGAGTTCGAGGCTCTTATG 660
QY 661 GAGCGCGCGCACAAAGCGGCGAGCGCGAGAGATTCGCGGCGGTTCGAGTTCGAGTTCGAGTTCGAG 720
DB 661 GAGCGCGCGCACAAAGCGGCGAGCGCGAGAGATTCGCGGCGGTTCGAGTTCGAGTTCGAGTTCGAG 720
QY 721 GAGCGCGCGCACGCTGCGCGTTCGCGGAGCGAGCGAGCGAGTTCGAGTTCGAGTTCGAGTTCGAG 780
DB 721 GAGCGCGCGCACGCTGCGCGTTCGCGGAGCGAGCGAGCGAGTTCGAGTTCGAGTTCGAGTTCGAG 780
QY 781 TCGGAGTCAITGCGGCTCGCGAGCTTCGCGAGAGTTCGCGAGTTCGCGAGTTCGCGAGTTCGCGAG 840
DB 781 TCGGAGTCAITGCGGCTCGCGAGCTTCGCGAGAGTTCGCGAGTTCGCGAGTTCGCGAGTTCGCGAG 840
QY 841 GCGCGGCTGCTGAGGCGCTTCGAGCGGCGCTTCAGCGGCTTCAGCGGCTTCAGCGGCTTCAGCGG 900
DB 841 GCGCGGCTGCTGAGGCGCTTCAGCGGCGCTTCAGCGGCTTCAGCGGCTTCAGCGGCTTCAGCGG 900
QY 901 GCGCTGCGCGCGCTGCGCGAGCTTCAGCGGCGCGCGCGAGCGAGCGAGCTTCGCTTCAGCGCG 960
DB 901 GCGCTGCGCGCGCTGCGCGAGCTTCAGCGGCGCGCGCGAGCGAGCGAGCTTCGCTTCAGCGCG 960
QY 961 GCGGATTCGCGCGAGCTTCGCGCGCGCGCGCGAGCGAGCGAGCTTCGCTTCAGCGCG 1020
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DB 1021 GCGGCTTCGAGTTCGAGCGCGCGCGCGAGCTTCAGCGGCTTCGAGTTCGAGTTCGAGTTCGAG 1080
QY 1081 GCGGCGCGCGAGAGGCTGCGAGCTTCGAGAGAGTTCGCTTCGCGGCTTCGAGTTCGAGTTCGAG 1140
DB 1081 GCGGCGCGCGAGAGGCTGCGAGCTTCGAGAGAGTTCGCTTCGCGGCTTCGAGTTCGAGTTCGAG 1140
QY 1141 TCGGTAGTACAGTTCGCGCGCGCTTCGCGTTCGCGAGAGAGTTCAGCGCTTCGCGTTCGAGCG 1200
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QY 1201 GCGCGCGCGCGCTAGCTGAGTTCGCGCGAGCGGCTTCGCGAGCTTCGAGGCTTCAGGG 1260
DB 1201 GCGCGCGCGCGCTAGCTGAGTTCGCGCGAGCGGCTTCGCGAGCTTCGAGGCTTCAGGG 1260
QY 1261 CACGCGCACCGCGCGCTTCGCGCTTCGAGCGCGAGCGGCTTCGAGGAGAGCGCGAGCTTCAGGG 1320
DB 1261 CACGCGCACCGCGCGCTTCGCGCTTCGAGCGCGAGCGGCTTCGAGGAGAGCGCGAGCTTCAGGG 1320
QY 1321 CACGCGCTTCGAGTTCGAGCGCGAGCGGCTTCGAGGAGAGCGCGAGCGCGAGCGCGAGCGCG 1380
DB 1321 CACGCGCTTCGAGTTCGAGCGCGAGCGGCTTCGAGGAGAGCGCGAGCGCGAGCGCGAGCGCG 1380
QY 1381 AGGCGCGCGAGCGCGCGCGCGAGCGCGCTTCGCGGAGCGGCTTCGAGGAGAGCTTCAGGG 1440
DB 1381 AGGCGCGCGAGCGCGCGCGCGAGCGCGCTTCGCGGAGCGGCTTCGAGGAGAGCTTCAGGG 1440
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DB 1441 CTGCTTCGCGCTTCGAGGAGAGAGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGTTC 1500

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D5 1501 AGGCTCTGGTACTGGCTCCCGAGACTGCTGGCCACAGATGGTGGTGGTGGTACT 1560
QY 1561 ATCAATAAAGATATTAACCAAC 1584
D5 1561 ATCAATAAAGATATTAACCAAC 1584

RESULT 2

AAF93866
ID AAF93866 standard; cDNA; 1584 BP.
AC AAF93866;
XX
DT 23-MAY-2001 (first entry)
XX
DE Human cDNA encoding a membrane or secretory protein clone F5EC0220.
XX
XX Human; secretory protein; membrane protein; vaccine; gene therapy;
KW rheumatoid arthritis; diabetes; ss.
XX
OS Homo sapiens.
XX
FN EP1067182-A2.
XX
PD 10-JAN-2001.
XX
PF 07-JUL-2000; 2000EP-0014090.
XX
PR 08-JUL-1999; 99JP-00194179.
PR 11-JAN-2000; 2000JP-00118775.
PR 02-MAY-2000; 2000JP-00183766.
XX
XX (HELI-) HELIX RES INST.
XX
XX Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;
XX
XX WPI: 2001-053989/11.
XX
XX P-PSDB; AAB88439.
XX

PT Nucleic acids encoding secretory proteins/membrane proteins, useful in
PT gene therapy or as candidate target molecules in drug development.
XX
XX Claim 1; SEQ ID NO 245; 609pp + Sequence Listing; English.
XX

CC This invention relates to nucleic acid sequences AAF93744 - AAF93916
CC which encode human secretory or membrane proteins represented by AAB88317
CC - AAB88419. Included in the invention are primers AAF93917 - AAF94295 and
CC AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the
CC invention. The invention also includes methods for the production of
CC antibodies directed against the proteins, and cDNA sequences, which can
CC be used in vaccines. The polynucleotide sequences can be used in gene
CC therapy. The polynucleotide sequences and the proteins they encode may be
CC used in the prevention, treatment and diagnosis of diseases associated
CC with inappropriate secretory protein/membrane protein expression. The
CC nucleic acids and complementary sequences may also be used as DNA probes
CC in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect
CC and quantitate the presence of similar nucleic acid sequences in samples.
CC They may also be used to study the expression and function of secretory
CC proteins/membrane polypeptides and their role in metabolism. The
CC polypeptides may be used as antigens in the production of antibodies
CC against them and in assays to identify modulators (agonists and

CC antagonists) of expression and activity. The antibodies and antagonists
CC may also be used as therapeutic agents to down regulate expression and
CC activity. The antibodies may also be used as diagnostic agents for
CC detecting the presence of the polypeptides in samples (e.g. by enzyme
CC linked immunosorbent assay (ELISA)). Examples of diseases which may be
CC treated include rheumatoid arthritis and diabetes
XX

SQ Sequence 1584 BP; 245 A; 572 C; 531 G; 236 T; 0 U; 0 Other;

Query Match 100.0%; Score 1584; DB 5; Length 1584;
Best Local Similarity 100.0%; Pred. No. 2.3e-277;
Matches 1584; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCTGCGCGCTGCGACTGAGAGCCCGGGCCCTCGGGCGCGCGGTTCCGCCCGCGAGCC 60
D5 1 GCCTGCGCGCTGCGACTGAGAGCCCGGGCCCTCGGGCGCGCGGTTCCGCCCGCGAGCC 60
QY 61 TCGCCCTTCGCCACACCCCGGGCGCGGTAGGGGGGTACAGATCTGCGCGCCCTTACCTTC 120
D5 61 TCGCCCTTCGCCACACCCCGGGCGCGGTAGGGGGGTACAGATCTGCGCGCCCTTACCTTC 120
QY 121 CGCCTCGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
D5 121 CGCCTCGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
QY 181 GCTGTGGCGAGCCCTTGTGTTATGAGACCTACAGATCTGCGAGAGCGCGGGGCTG 240
D5 181 GCTGTGGCGAGCCCTTGTGTTATGAGACCTACAGATCTGCGAGAGCGCGGGGCTG 240
QY 241 GCGGCGCGGCGAGCGCGGCTGCTGCGAGGCTGAGCGCGGAGTGGTGGCAGAGTCTCGG 300
D5 241 GCGGCGCGGCGAGCGCGGCTGCTGCGAGGCTGAGCGCGGAGTGGTGGCAGAGTCTCGG 300
QY 301 GCGCGCGCGCTCGGGGTGCGAGAGTGCAGATTCAGTTCGGCTTCGCCGCGCTGGAATTC 360
D5 301 GCGCGCGCGCTCGGGGTGCGAGAGTGCAGATTCAGTTCGGCTTCGCCGCGCTGGAATTC 360
QY 361 TCAGCGACACAGAGGCTTTGAGCGCATCTGCAACAGGACATTGCGGAGACGGCTTC 420
D5 361 TCAGCGACACAGAGGCTTTGAGCGCATCTGCAACAGGACATTGCGGAGACGGCTTC 420
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D5 421 GTGTTGCGCATCACTCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
QY 481 GAGCTGCTGCACTGCG 540
D5 481 GAGCTGCTGCACTGCG 540
QY 541 CTGCG 600
D5 541 CTGCG 600
QY 601 GAGTGGGAGGCTGCG 660
D5 601 GAGTGGGAGGCTGCG 660
QY 661 GACG 720
D5 661 GACG 720
QY 721 GAGGCGGCGCGCGCTGCG 780
D5 721 GAGGCGGCGCGCGCTGCG 780

AC	ABX75316;
XX	
XX	25-MAR-2003 (first entry)
DT	
DI	
DE	Human cDNA encoding WNT-6.
XX	
XX	Gene; Notch; Wnt; embryonic stem cell; embryogenesis; ss;
KW	differentiation; ligand; Parkinson's disease; Huntington's disease;
KW	motor neuron disease; heart disease; diabetes; liver disease; human;
KW	cirrhosis; renal disease; AIDS; acquired immunodeficiency syndrome.
XX	
OS	Homo sapiens.
XX	
XX	W0200277204-A2.
XX	
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XX	25-MAR-2002; 2002WC-GB001195.
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XX	23-MAR-2001; 2001GB-00007296.
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XX	23-MAR-2001; 2001GB-00007299.
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XX	17-APR-2001; 2001GB-00009346.
XX	
XX	(AXOR-) AXORDIA LTD.
XX	
XX	Andrews P, Walsh J, Gokhale P;
XX	
XX	WPI; 2003-C92852/08.
XX	
XX	P-PSDB; ABU5888.
XX	
XX	Modulating the differentiation of embryonic stem cells by providing
XX	ligands which bind receptors in the Notch and Wnt pathways, useful for
XX	treating diseases such as Parkinson's, Huntington's, heart disease,
XX	diabetes and AIDS.
XX	
XX	Claim 3; Fig 42; 12pp; English.
XX	
XX	The invention relates to modulating the differentiation of an embryonic
XX	stem cell, comprising: (a) providing a culture of embryonic stem cells;
XX	(b) providing at least one ligand or its active binding fragment, capable
XX	of binding its cognate receptor polypeptide expressed by the embryonic
XX	stem cell; (c) forming a culture comprising embryonic stem cells and the
XX	ligand; and (d) growing the cell culture. Also included are: (i)
XX	Modulating the differentiation of embryonic stem cells, comprising: (a)
XX	providing a cell transfected with a nucleic acid molecule selected from:
XX	(i) any of 9 fully defined Wnt nucleic acid sequences; (ii) a nucleic
XX	acid molecule that hybridises to the nucleic acid in (i), and which
XX	encodes a ligand capable of modulating embryonic stem cell
XX	differentiation, or capable of binding a Wnt receptor; or (iii) nucleic
XX	acid molecules which are degenerate as a result of the genetic code to
XX	the sequences of (i) or (ii); (b) Forming a culture comprising the cell
XX	identified in (a) with an embryonic stem cell; and (c) growing the
XX	culture for the maintenance and/or differentiation of the embryonic stem
XX	cell; (2) Inhibiting the differentiation of embryonic stem cells,
XX	comprising: (a) providing at least one polypeptide of its active
XX	fragment, that are inhibitors of the Wnt signalling pathway; (b) forming
XX	a culture comprising the cell identified in (a) with an embryonic stem
XX	cell; and (c) growing the culture for the maintenance of embryonic stem
XX	cells in an undifferentiated state; or (3) Inhibiting the differentiation
XX	of embryonic stem cells, comprising: (a) providing a cell transfected
XX	with a nucleic acid molecule selected from: (i) a molecule encoding a Wnt
XX	inhibitory polypeptide; (ii) a molecule which hybridises to the molecule
XX	of (i) and encodes a polypeptide capable of inhibiting Wnt signalling;

XX	Ligand; WNT-5b; stem cell; stem-loop RNA; anti-naemic; cerebroprotective;
XX	neuroprotective; neurotropic; antiparkinsonian; cardiast; hepatotropic;
XX	antidiabetic; vulnary; gene therapy; gene; ds.
XX	Unidentified.
XX	WO2003012082-A2.
XX	13-FEB-2003.
XX	25-JUL-2002; 2002WO-GE003409.
XX	26-JUL-2001; 2001GB-00018223.
XX	(AXOR-) AXORDIA LTD.
XX	Andrews P, Walsh J, Gokhale P;
XX	WPI; 2003-278398/27.
XX	Modulating the differentiation state of a stem cell, useful for treating
XX	e.g. pernicious anemia, strokes, cirrhosis, diabetes or a
XX	neurodegenerative disease, comprises contacting a stem cell with a stem
XX	loop RNA.
XX	Claim 7; Fig 23; 65pp; English.
XX	The present sequence is the nucleic acid sequence of ligand WNT-5A. The
XX	invention relates to a method of modulating the differentiation state of
XX	a stem cell, such as an embryonic stem cell, embryonic germ cell,
XX	embryonal carcinoma cell, hematopoietic stem cell, muscle stem cell,
XX	nerve stem cell, skin dermal sheath stem cell, liver stem cell or
XX	teratocarcinoma cell. The method involves contacting the stem cell with a
XX	stem-loop RNA molecule or a nucleic acid molecule or vector encoding the
XX	stem-loop RNA, where the nucleic acid is preferably derived from one of
XX	the nucleic acid sequences in AB281794-844, including the present
XX	sequence, and may encode a cell surface receptor expressed by a stem
XX	cell, or a ligand. The RNA molecule, the nucleic acid molecule or the
XX	vector is useful for promoting the differentiation of stem cells and for
XX	providing differentiated cells/tissues for the treatment of diseases in
XX	which cell/tissues are destroyed by the disease. These diseases include
XX	pernicious anaemia, stroke, neurodegenerative diseases such as
XX	Parkinson's disease and Alzheimer's disease, coronary heart disease,
XX	cirrhosis, diabetes, or nerve damage as a consequence of trauma (e.g.
XX	replacement of spinal cord tissue) (claimed)
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Best Local Similarity	99.8%	Pred. No. 3.9e-276;		
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DT	11-JUN-2003 (first entry)
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9 1434.4 90.6 1754 10 US-09-999-570-85 Sequence 85, Appl
10 1434.4 90.6 1754 14 US-10-000-489-83 Sequence 83, Appl
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12 1434.4 90.6 1754 14 US-10-000-986-83 Sequence 83, Appl
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16 1434.4 90.6 1754 14 US-10-001-142-83 Sequence 85, Appl
17 1434.4 90.6 1754 14 US-10-001-142-85 Sequence 97, Appl
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24 1333.8 84.2 1855 14 US-10-154-678-97 Sequence 97, Appl
25 1333.8 84.2 1855 14 US-10-001-142-97 Sequence 97, Appl
26 466.6 29.5 803 9 US-09-764-903-24 Sequence 24, Appl
27 466.6 29.5 803 14 US-10-091-391-24 Sequence 24, Appl
28 347.4 21.9 499 9 US-09-833-381-206 Sequence 206, App
29 287 18.1 402 9 US-09-833-381-1448 Sequence 1448, A
30 213.2 13.5 1198 14 US-10-285-976-12 Sequence 12, Appl
31 213.2 13.5 1202 9 US-09-764-903-23 Sequence 23, Appl
32 213.2 13.5 1202 14 US-10-091-391-28 Sequence 28, Appl
33 213.2 13.5 1515 13 US-10-002-600-54 Sequence 54, Appl
34 213.2 13.5 1598 13 US-10-098-841-251 Sequence 251, App
35 211.6 13.4 2049 9 US-09-978-295A-225 Sequence 225, App
36 211.6 13.4 2049 9 US-09-978-697-225 Sequence 225, App
37 211.6 13.4 2049 9 US-09-978-192A-225 Sequence 225, App
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ALIGNMENTS

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; Publication No. US20030165500A1
; GENERAL INFORMATION:
; APPLICANT: Rhee, Chae-Seo
; APPLICANT: Malini, Sen
; APPLICANT: Wu, Christina
; APPLICANT: Leoni, Lorenzo M.
; APPLICANT: Carr, Maripat
; APPLICANT: Carson, Dennis A.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Wnt and Frizzled Receptors as targets for Immunotherapy
; FILE REFERENCE: 023070-130320US
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/287,995

; PRIOR FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: WO PCT/US02/13802
; PRIOR FILING DATE: 2002-05-01
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 1726
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Wnt-6
US-10-285-976-18

Query Match 99.6%; Score 1577.2; DB 14; Length 1726;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1579; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 61 TCGCGCGCTCG 120
DB 185 TCGCGCGCTCG 244
QY 121 CGCGCTCGCGCGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
DB 245 CGCGCTCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 304
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DB 365 GCGCGCGCGCGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 424
QY 301 GCGCGCGCGCGCTCG 360
DB 425 GCGCGCGCGCTCG 484
QY 361 TCCAGCGCACGAGAGCGCGCTTTGAGCGCAFOCTTSCAAGAGCAATTCGGGAGAGCG 420
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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	2997	99.3	3045	6	BD156664 Primer fo
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8	2987	98.0	3042	9	AF236056 Homo sapi
9	2979	96.8	3031	9	BC001740 Homo sapi
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ALIGNMENTS

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VERSION AX136405.1 GI:14272809
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ota,T., Isegai,T., Nishi,Kawa,T., Kawai,Y., Sugiyama,T. and
Hayashi,K.
TITLE Secretory protein or membrane protein
JOURNAL Patent: EP 1067182-A 327 10--JAN-2001;
Helix Research Institute (JP)
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ORIGIN

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Query Match 100.0%; Score 3017; DB 6; Length 3017;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTGGGCGCACGGGCGGAGCGCGGCGGAGCTCGAGCGCGGCGGCGGAGAGCGCAAC 60
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QY 61 CGGCGCGGCTCGTAGCGGCGGCGCGCGGATCCCGAGTGGCGGCGGAGCGCTCGAAAAGA 120
DB 61 CGGCGCGGCTCGTAGCGGCGGCGCGCGGATCCCGAGTGGCGGCGGAGCGCTCGAAAAGA 120

QY 121 TTCTCAGCGCTGATTTTGAGTGTATGGCTTGGGAAAGCGGCGTGGCAGCATGAAGTCGC 180
DB 121 TTCTCAGCGCTGATTTTGAGTGTATGGCTTGGGAAAGCGGCGTGGCAGCATGAAGTCGC 180

QY 181 CGGCGCGCTGCTGCTGGCGCGCTGGTGGCGCTGCATCATCTCTTGGGCTTCAACTACTGGA 240
DB 181 CGGCGCGCTGCTGCTGGCGCGCTGGTGGCGCTGCATCATCTCTTGGGCTTCAACTACTGGA 240

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QY 301 GCAAGCGGCTCGAGAGAGAGCGCGCTGGAGCTGAAAGAGAAACAGTTCACAGGAGAGC 360
DB 301 GCAAGCGGCTCGAGAGAGAGCGCGCTGGAGCTGAAAGAGAAACAGTTCACAGGAGAGC 360

QY 361 TGGAGAAAGCAAGCGGAGAGAGCTTGACAAATCCAGTCCAGGCAAACTTCCAGCTGAGA 420
DB 361 TGGAGAAAGCAAGCGGAGAGAGCTTGACAAATCCAGTCCAGGCAAACTTCCAGCTGAGA 420

QY 421 GCGTCAACAGCTGTACCAGAGAGAAAGGCGTTTGTGATACATCACTACAGAGTTC 480
DB 421 GCGTCAACAGCTGTACCAGAGAGAAAGGCGTTTGTGATACATCACTACAGAGTTC 480

QY 481 AGAGGCTCATCCGAGTGTCTGAGAGACCAAGTAAAGACCTTCAGAGAGAAATACCGAGGC 540
DB 481 AGAGGCTCATCCGAGTGTCTGAGAGACCAAGTAAAGACCTTCAGAGAGAAATACCGAGGC 540

QY 541 TCGAGCAGAGTGTCTTCAGTTCAGAGAAACAGACCACTGAGAGAGAAATTCCTCT 600
DB 541 TCGAGCAGAGTGTCTTCAGTTCAGAGAAACAGACCACTGAGAGAGAAATTCCTCT 600

QY 601 ACGACCTGAGCCAGTGCATCAATCAGATGAAGGAGTGAAGAACAGTGTGAGGAGGAA 660
DB 601 ACGACCTGAGCCAGTGCATCAATCAGATGAAGGAGTGAAGAACAGTGTGAGGAGGAA 660

QY 661 TAGAAGAGTTCACAAAAGGGGAATGAAAGTGTAGCTTCCAGAGACCTGAGTGAAGA 720
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DB 721 ACGACCGAGACAGCAGCTCCAGGCGCTCAGTGAAGCGCTCAGCCCGCTGAGGAGCAG 780

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DB 781 GCTTGCACACACAGAGTGCACAAAGGAGGAGAAAGCTGCTTGGTAAACAACAAAGTCCC 840

QY 841 AGACACAGCGCCCGAGTTCGGAAGTGGTTTGGATTCAAAGAGACAAAGTTGAGAAAGG 900
DB 841 AGACACAGCGCCCGAGTTCGGAAGTGGTTTGGATTCAAAGAGACAAAGTTGAGAAAGG 900

QY 901 AAACCAATGATCCAGTGGTGAATGAGAGAGCTCAGAGGAGCAGAGCTGCCGAGGAGC 960
DB 901 AAACCAATGATCCAGTGGTGAATGAGAGAGCTCAGAGGAGCAGAGCTGCCGAGGAGC 960

QY 961 CAGGCGGAGAGAGAGTGGTGGAAAGACACCTGTAGGTGGAAGAGAGGCTTGGGGGAGAGC 1020
DB 961 CAGGCGGAGAGAGAGTGGTGGAAAGACACCTGTAGGTGGAAGAGAGGCTTGGGGGAGAGC 1020

QY 1021 GAGAACTGGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
DB 1021 GAGAACTGGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080

QY 1081 AGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
DB 1081 AGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140

QY 1141 AAGCTGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
DB 1141 AAGCTGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200

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RESULT 2	BD093297	LOCUS	3017 bp	DNA	linear	PAT 27-AUG-2002
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ACCESSION	BD093297					
VERSION	BD093297.1	GI:22638865				
KEYWORDS	WO 0104299-A/4.					
SOURCE	Human sapiens (human)					
ORGANISM	Human sapiens					
REFERENCE	1	(bases 1 to 3017)				
AUTHORS	Ota,T., Isogai,T., Nishikawa,T., Kawai,S., Yamazaki,M., Sato,S., Arakawa,H. and Morita,M.					
TITLE	Amoyloid beta aglilation regulatory factor					
JOURNAL	Patent: WO 0104299-A 4 18-JAN-2001;					
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COMMENT	OS Homo sapiens (human)					
	PN WO 0104299-A/4					
	PD 18-JAN-2001					
	PE 06-JUL-2000	WO 2000JP04515				
	PR 08-JUL-1999	JP 99P 194179,18-OCT-1999	US 60/159586	PI		
	TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,YURI KAWAI,MAYAKO YAMAZAKI,					
	YAMAZAKI,					
	PI SUSUMU SATO,HIROYUKI ARAKAWA,MASAHIKO MORITA					
	PC C12N15/12,C07K14/47,C07K16/18,C12N5/10,A61K45/00,A61K48/00,PC A61K31/711,					
	PC A61P25/28,G01N33/15,G01N33/50					
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FR	FR	CDS	(141)..(1343).			
FT	FT	CDS	Location/Qualifiers			
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		/db_xref="taxon:9606"				
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	Best Local Similarity	100.0%;	Pred. No. 0;			
	Matches 3017;	Conservative	0;	Mismatches	0;	Gaps 0;
Qy	1	GCTGGGCGGCA CGGCGCGGA GCGCGCGGAGCTCGAGCGCGGCGGCGGCGGAGAGGAC	60			
Db	1	GCTGGGCGCACGCGCGGA GCGCGCGGAGACTCGAGGCGGCGGCGGCGGAGAGGAC	60			
Qy	61	CGGGCGGCTCGTAGCGGGGCGCGGATCCCGAGTGGCGGGCCGAGACCTCGAAAGAGA	120			
Db	61	CGGGCGGCTCGTAGCGGGGCGCGGATCCCGAGTGGCGGGCCGAGACCTCGAAAGAGA	120			
Qy	121	TTCTCAGCGCTGATTTCGAGATGATGGGCTTGGGAAACGGGGGTTCGACGATGAAGTCGC	180			
Db	121	TTCTCAGCGCTGATTTCGAGATGATGGGCTTGGGAAACGGGGGTTCGACGATGAAGTCGC	180			
Qy	181	CGGCGCTCGTGGCGGCGCTGGTGGGCTTGCATCGTCTTGGGCTTCGACTACTGGA	240			
Db	181	CGGCGCTCGTGGCGGCGCTGGTGGGCTTGCATCGTCTTGGGCTTCGACTACTGGA	240			
Qy	241	TTGGAGACTCCCGGAGCGTGGAGCTCGACGACGAGATCATGAGCTGGAAGGCGAGGTC	300			
Db	241	TTGCGAGCTCCCGGAGCGTGGAGCTCGACGACGAGATCATGAGCTGGAAGGCGAGGTC	300			

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 Db 2221 ACTTTATCTGAGTAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 2280
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 BD123655 3017 bp DNA linear PAF 18-SEP-2002

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DEFINITION AK075542
ACCESSION AK075542.1 GI:22761755
VERSION AK075542.1
KEYWORDS oligo capping; fls (full insert sequence).
SOURCE Homo sapiens (human)

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RESULT 5
AX877451 3045 bp DNA linear PAT 17-DEC-2003
LOCUS Sequence 12356 from Patent EP1074617.
DEFINITION AX877451
ACCESSION AX877451.1 GI:40032187
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 Ota, T., Inagai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.,
AUTHORS Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.
TITLE Primers for synthesizing full-length cDNA and their use
JOURNAL Patent: EP 1074617-A 12356 07-FEB-2001;
Research Association for Biotechnology (JP)
FEATURES
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170..1375
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EQVEDPVGSGFGGELGQTPQVQALSVSQENPEHGPEDDLVLPDQEEQEE
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Query Match 99.3%; Score 2997; DB 6; Length 3045;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3011; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
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RESULT 6
BD156664

RESULT 6
BD156664

LOCUS BD156664 3045 bp DNA linear PAT 17-JUN-2003
DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION BD156664
VERSION BD156664.1 GI:27862422
KEYWORDS JP 2002191363-A/11507.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 3045)
Ota,T., Isozaki,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002191363-A 11507 09-JUL-2002;
HELIX RESEARCH INSTITUTE
CS Homo sapiens (human)
PN JP 2002191363-A/11507
PD 09-JUL-2002
PF 28-JUL-2000 JP 200280990
PI TOSHIO OTA, TAKAO ISOZAKI, TETSUO NISHIKAWA, KOJI HAYASHI, KAZUHI
SAITO,
PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
PI KENICHI NAGAI, TETSUJI OTSUKI
PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
10, C12P21/02, C12Q1/68, C12P21/09, G06F17/30, C12N15/00, C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH Key

LOCATION/Qualifiers
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Query Match 99.3%; Score 2997; DB 6; Length 3045;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3011; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
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QY 841 AGAGCCTGAGCCAGTGCATCAATCAGATGAAGAGGCTGAGGAAACAGTGTGAGAGAGGAA 900
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VERSION	AK027717.1	GI:14042605	
KEYWORDS	oligo capping; fls (full insert sequence).		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1		
AUTHORS	Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y., Nishikawa,T., Nagai,K., Sugano,S., Ishibashi,T., Fujimori,K., Teraai,H., Kmata,M., Watanabe,M., Hirakawa,S., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagahara,K., Masuho,Y. and Kanehori,K.		
TITLE	NEDO human cDNA sequencing project		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 3045)		
AUTHORS	Isogai,T. and Otsuki,T.		
TITLE	Direct Submission		
JOURNAL	Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:82-0812-3986)		
COMMENT	NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology; cDNA library construction; 5'- & 3'-end one pass sequencing and clone selection; Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.		
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	Query Match 99.3%; Score 2997; DB 9; Length 3045;		
	Best Local Similarity 99.8%; Pred. No. 0;		
	Matches 3011; Conservative 0; Mismatches 1; Gaps 1;		
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2909	TCTCTCTCCAGCTCAGTTGAGTCTCTCTGGGGTGTATAGGAATTTCTCTTCTGCTTTC	2968
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2969	TCAATTAAGTCTCATTGATCTCATGTTTAAATTTGTACGCATAGAAATTCCTGAGAAATA	3028
3001	AATGTCTCTTCAACTT	3017
3029	AATGTCTCTTCAACTT	3045

RESULT 8
AF236056

LOCUS	AF236056	3042 bp	mRNA	linear	PRI 08-JUN-2000
DEFINITION	Homo sapiens golgi membrane protein GP73 mRNA, complete cds.				
ACCESSION	AF236056				
VERSION	AF236056.1	GI:7271566			
KEYWORDS	.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 3042)				
AUTHORS	Kladney R.D., Bulla, G.A., Guo, L., Mason, A.L., Tollefson, A.E., Simon, D.J., Koutoubi, Z., and Fimmel, C.J.				
TITLE	GP73, a novel Golgi-localized protein upregulated by viral infection				
JOURNAL	Gene 249 (1-2), 53-65 (2000)				
MEDLINE	20293047				
PubMed	10831838				
REFERENCE	2 (bases 1 to 3042)				
AUTHORS	Fimmel, C.J. and Kladney, R.D.				
TITLE	Direct Submission				
JOURNAL	Submitted (16-FEB-2000) Internal Medicine, St. Louis University, 3635 Vista Ave. at Grand Blvd., St. Louis, MO 63110-0250, USA				
FEATURES	<p>Location/Qualifiers</p> <p>1..3042</p> <p>/organism="Homo sapiens"</p> <p>/mol_type="mRNA"</p> <p>/db_xref="taxon:9606"</p> <p>/chromosome="9"</p> <p>/note="upregulated in adult syncytial giant-cell hepatitis"</p> <p>151..1353</p> <p>/codon_start=1</p> <p>/product="golgi membrane protein GP73"</p> <p>/protein_id="AAF44663.1"</p> <p>/db_xref="GI:7271867"</p> <p>/translation="MGLNGRRSKSPVLVLAIVACIVLGFNVWASSRSVDLQTRIMELGQVRRRAAEAGVAKLVKEVQGELEKORGLDKIOSSHNFQESVVKLYODEAVLWNNITGGERLIVLQDQLTKQVNTGLQDVLQFQKNTLRLKESYDLSSCHIQMFVEQCEERTVEVTKGNEANASRLSDNDQQLQALISEPFLQAGLPHIEVPGKNGVLNKSSTPQVSRVLELDRVKEKEINEIQVNEBPRDLRQPEFGREQVYDPRVGGSGAGAGELGQTPQVAAALSVPENPEMGEPRDLVTPDQEEQEEQASGRNQKLREGDDYNNDEANESEITDKQAAGADNDIDVENVEDQKRDITLLIDQREKRHH1"</p> <p>178</p> <p>/note="alternate position for initiation methionine"</p>				
misc_feature					
polya_signal	1448..1453				
polya_signal	2950..2955				
polya_signal	3003..3008				
ORIGIN					
Query Match	99.0%; Score 2987.6; DB 9; Length 3042;				
Best local Similarity	99.8%; Pred. No. 0;				
Matches 3012;	Conservative 0; Mismatches 4; Indels 2; Gaps 2;				
QY	1 GCTGGCGGCACGGCGGAGCGCGGCGGAGCTCGAGCCGGCGGCGGAGAGCGACC 60				
DB	8 GCTGGCGGCACGGCGGAGCGCGGCGGAGCTCGAGCCGGCGGCGGAGAGCGACC 67				
QY	61 CGGGCGGGCTCGTAGCGGCGCGCGCGGATCCCGAGTGGCGGCGGAGCGCTCGAAAAGAGA 120				
DB	68 CGGGCGGGCTCGTAGCGGCGCGCGCGGATCCCGAGTGGCGGCGGAGCGCTCGAAAAGAGA 127				
QY	121 TTCTCAGCGCTGATTTTGAGATGATGGCGTTGGGAAAGCGGCGCTCGCGAGATGAAGTGGC 190				

QY 1081 AGATGAGGGCCCTGAGCGAGACAGAGCTTGTCTCCCGGAGGAGAGGAGCGA55 1140
D6
QY 1086 AGATGAGGGCCCTGAGCGAGACAGAGCTTGTCTCCCGGAGGAGAGGAGCGA53 1147
D6
QY 1141 AAGCTGCCGGGAGAGGAGAAAACGAGAGAACTGAGAGGAGAGATGATACAACTGG 1200
D6 1148 AAGCTGCCGGGAGAGGAGAAAACGAGAGAACTGAGAGGAGAGATGATACAACTGG 1207
QY 1201 ATGAAATGAAGCAGATCTTGAGACAGAGAAAGAGAGCCCTGGCAGGGAATGACAGAA 1260
D6 1208 ATGAAATGAAGCAGATCTTGAGACAGAGAAAGAGAGCCCTGGCAGGGAATGACAGAA 1267
QY 1261 ACATAGATGTTTTTAATGTGAAGATCAGAAAGACACCAATTAATTTACTTGAATGAGC 1320
D6 1268 ACATAGATGTTTTTAATGTGAAGATCAGAAAGACACCAATTAATTTACTTGAATGAGC 1327
QY 1321 GTGAAAACGGATCAATACACTGTGAATGAACTGGAATCACAATTTACAGACAGGGCC 1380
D6 1328 GTGAAAACGGATCAATACACTGTGAATGAACTGGAATCACAATTTACAGACAGGGCC 1387
QY 1381 GAAGAGATGACTTTAAATGTTTATGAGGGAAGTGAATGAACTGGAATGTAATA 1440
D6 1388 GAAGAGATGACTTTAAATGTTTATGAGGGAAGTGAATGAACTGGAATGTAATA 1447
QY 1441 AATAAATGTACATCTGAAGATGATTAATGTGAATTTAGTAGGACTTGTGAGAA 1500
D6 1448 AATAAATGTACATCTGAAGATGATTAATGTGAATTTAGTAGGACTTGTGAGAA 1507
QY 1501 AATAAGGAATGTTTAAACAGCTTTTGGGGGGTACTTTGGAATGCTAATAAGGT 1559
D6 1508 AATAAGGAATGTTTAAACAGCTTTTGGGGGGTACTTTGGAATGCTAATAAGGT 1567
QY 1560 GTCAAAATTTTGTAGTAGTATTCGTGAGAGCTCAACAGCAAACTGGAACATAGT 1619
D6 1568 GTCAAAATTTTGTAGTAGTATTCGTGAGAGCTCAACAGCAAACTGGAACATAGT 1627
QY 1620 TCTCCTTCAAGTGTGGGAGAGAGGGGGCTTCTGATCTGGAATTAACCTTTGTAAA 1679
D6 1628 TCTCCTTCAAGTGTGGGAGAGAGGGGGCTTCTGATCTGGAATTAACCTTTGTAAA 1687
QY 1680 TTAACAGCCCACTATAGAGAGTCCATCTGCTGAGAGAGAGACAGAACTCTGGTT 1739
D6 1688 TTAACAGCCCACTATAGAGAGTCCATCTGCTGAGAGAGAGACAGAACTCTGGTT 1747
QY 1740 CGGTCTGCTCTCCAGCTGCTGACCAAGTGTGGTGGCAGCCCTGTTACCTGTTCTCAT 1799
D6 1748 CGGTCTGCTCTCCAGCTGCTGACCAAGTGTGGTGGCAGCCCTGTTACCTGTTCTCAT 1807
QY 1800 GAAAATGTGGCTAATGCTCTTGTGTAGTCACTTCTGATCTGACAACTCAATCAAT 1859
D6 1808 GAAAATGTGGCTAATGCTCTTGTGTAGTCACTTCTGATCTGACAACTCAATCAAT 1867
QY 1860 GGGCTAGAGCACTGACTGTTAACACAAAGCTCACTAGCAAAAGTAGCAAGCTTTAAGTC 1919
D6 1868 GGGCTAGAGCACTGACTGTTAACACAAAGCTCACTAGCAAAAGTAGCAAGCTTTAAGTC 1927
QY 1920 TAAATACAAAGCTGTCTGTGTGAGATTTTAAAGGCTACTGTATTAATAACCCCTG 1979
D6 1928 TAAATACAAAGCTGTCTGTGTGAGATTTTAAAGGCTACTGTATTAATAACCCCTG 1987
QY 1980 TCAATTTTAAATGTACAAAACGCTATTAAGTGGCTTAGAATTTGAATTTGTGCTTTA 2039
D6 1988 TCAATTTTAAATGTACAAAACGCTATTAAGTGGCTTAGAATTTGAATTTGTGCTTTA 2047

QY 2040 TTTACTTTGCTTCTGTGTGGGCAAGCACTCTTCCCTAAATATATATTAATTAACAGAAA 2099
D6 2048 TTTACTTTGCTTCTGTGTGGGCAAGCACTCTTCCCTAAATATATATTAATTAACAGAAA 2107
QY 2100 ASCAAGAAGCAGATTAGGTTTTTGACAAAACAAACAGGCCCCAAAGGGGCTGACTGGAG 2159
D6 2108 ASCAAGAAGCAGATTAGGTTTTTGACAAAACAAACAGGCCCCAAAGGGGCTGACTGGAG 2167
QY 2160 CAGAGCATGGTGAAGGCAAGGCATGAGAGGCAAGTTTTGTTGTGACAGATCTGTGCC 2219
D6 2168 CAGAGCATGGTGAAGGCAAGGCATGAGAGGCAAGTTTTGTTGTGACAGATCTGTGCC 2226
QY 2220 TACTTTACTTACTGAGTAAAGAAAACAAAGTTCATTGATGTCGAAGGATATAACAGTG 2279
D6 2227 TACTTTACTTACTGAGTAAAGAAAACAAAGTTCATTGATGTCGAAGGATATAACAGTG 2286
QY 2280 TTAGAATTAAGGACTGTTTAGAAAAACAGGAAACAAATGTTGTTTTTATCNAAGTGTAC 2339
D6 2287 TTAGAATTAAGGACTGTTTAGAAAAACAGGAAACAAATGTTGTTTTTATCNAAGTGTAC 2346
QY 2340 ACATTTAGCTTGTGTAATGACTCACAAAACGATTTTAAATCAGTAAATGTGAAT 2399
D6 2347 ACATTTAGCTTGTGTAATGACTCACAAAACGATTTTAAATCAGTAAATGTGAAT 2406
QY 2400 TTGAAAATTAAGTAAATCCTAATTCACAAATGCAATGCAATTAAGGTTTGAATGACT 2459
D6 2407 TTGAAAATTAAGTAAATCCTAATTCACAAATGCAATGCAATTAAGGTTTGAATGACT 2466
QY 2460 TGGTTCTTAGTATTAATTTATGTAATAGGCTCTTACCACTTGCNAATTAATGCGCACAT 2519
D6 2467 TGGTTCTTAGTATTAATTTATGTAATAGGCTCTTACCACTTGCNAATTAATGCGCACAT 2526
QY 2520 CATTAATGACTGACTCCACAGTAAGGCTCTTAAGGGGTAAAGTAGGAGATCCACAGAT 2579
D6 2527 CATTAATGACTGACTCCACAGTAAGGCTCTTAAGGGGTAAAGTAGGAGATCCACAGAT 2586
QY 2580 TTGAGATGCTAAAGGCCCCCAGAGATCGTTTGAACCAACCCCTTAATTTGAGAGGGGAAA 2639
D6 2587 TTGAGATGCTAAAGGCCCCCAGAGATCGTTTGAACCAACCCCTTAATTTGAGAGGGGAAA 2646
QY 2640 TGGGGCTTAGAAGTTACAGAGCATCTAGCTGGTGGGCTGGGACCCCTGGGCTCCACAGAG 2699
D6 2647 TGGGGCTTAGAAGTTACAGAGCATCTAGCTGGTGGGCTGGGACCCCTGGGCTCCACAGAG 2706
QY 2700 CTCCGAGTAGCTGGGACTACAGGCAACAGCTCACTGAAGGGGCTGTTTGCATTTCA 2759
D6 2707 CTCCGAGTAGCTGGGACTACAGGCAACAGCTCACTGAAGGGGCTGTTTGCATTTCA 2766
QY 2760 CGCTGCCACCTCCAACTTAACATTTCTCATATGTGATGCTCTTAGTCACTTAAGGTTAAA 2819
D6 2767 CGTGGCACCCTCCAACTTAACATTTCTCATATGTGATGCTCTTAGTCACTTAAGGTTAAA 2826
QY 2820 CTGTCGCCACCAAGAAAGGAACTTAGATTAATCTTAGAGTACTTTCTACTCTCTAA 2879
D6 2827 CTGTCGCCACCAAGAAAGGAACTTAGATTAATCTTAGAGTACTTTCTACTCTCTAA 2886
QY 2880 GTCCCTCTCCAGCTCACTTTGAGTCTCTTGGGTTTGAAGAAATTTCTCTTCTTT 2939
D6 2887 GTCCCTCTCCAGCTCACTTTGAGTCTCTTGGGTTTGAAGAAATTTCTCTTCTTT 2946
QY 2940 CTCATAAAGTCTCTATTCTCATCTCATGTTTAATTTGTACGATAGATGCTGAGAAATA 2999

OM nucleic - nucleic search, using sw model

Run on: April 2, 2004, 21:47:00 ; Search time 755.831 Seconds
(without alignments)

16957.243 Million cell updates/sec

Title: US-10-030-269A-7

Perfect score: 3017

Sequence: 1 gctgggcgcacgcggag.....taaaatgtctgttcaactt 3017

Scoring table: IDENTITY_NJC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: _geneseq1980s:*
2: _geneseq1990s:*
3: _geneseq2000s:*
4: _geneseq2001as:*
5: _geneseq2001bs:*
6: _geneseq2002s:*
7: _geneseq2003as:*
8: _geneseq2003bs:*
9: _geneseq2003cs:*
10: _geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query			DB	ID	Description
	Score	Match	Length			
1	3017	100.0	3017	4	AAF29360	Amyloid-b
2	3017	100.0	3017	5	AAF93907	Human cDN
3	2998.6	99.4	3051	3	AAC64559	Human pro
4	2998.6	99.4	3210	5	ABV25476	Human pro
5	2997	99.3	3045	4	AHL14672	Human cDN
6	2987.6	99.0	3042	7	ACC50169	Breast ca
7	2987.6	99.0	3042	9	ADB75331	Prostate
8	2987.6	99.0	3042	9	ADD18542	Human pro
9	2921.8	96.8	3154	6	ABQ99606	Human cod
10	2899.4	96.1	4042	7	ABZ35869	Human sec
11	2876	95.3	3174	3	AAA26421	Human cDN
12	2744.8	91.0	2962	9	AUB63189	Human cDN
13	2045	67.8	2143	2	AAZ42062	Human end

Search completed: April 3, 2004, 11:14:23
Job time : 7766.59 secs

14.4	1715.4	56.9	2654	6	ABS57323	cDNA enco
14.5	1427.4	47.3	1429	3	AAA37050	Human PRO
14.6	1427.4	47.3	1429	4	AAF54272	DNA encoed
14.7	1427.4	47.3	1429	4	AAS21486	Human cDN
14.8	1427.4	47.3	1429	7	ACD24095	Novel hum
14.9	1427.4	47.3	1429	7	ACA67236	cDNA enco
14.10	1427.4	47.3	1429	7	ACA03645	cDNA enco
14.11	1427.4	47.3	1429	7	ACB93983	DNA encoed
14.12	1427.4	47.3	1429	7	ACD42037	Human sec
14.13	1427.4	47.3	1429	7	ACA04266	Human cDN
14.14	1427.4	47.3	1429	8	ADA46004	Novel hum
14.15	1427.4	47.3	1429	8	ADA76435	Human PRO
14.16	1427.4	47.3	1429	8	ADA19085	Human PRO
14.17	1427.4	47.3	1429	8	ADA61708	Homo sapi
14.18	1427.4	47.3	1429	8	ADA61943	Novel hum
14.19	1427.4	47.3	1429	8	ADB19493	cDNA enco
14.20	1427.4	47.3	1429	8	ADB26034	cDNA enco
14.21	1427.4	47.3	1429	8	ADA86513	Novel hum
14.22	1427.4	47.3	1429	8	ADB16077	Human PRO
14.23	1427.4	47.3	1429	8	ADA47863	Human PRO
14.24	1427.4	47.3	1429	8	ACD68309	Novel hum
14.25	1427.4	47.3	1429	8	ADA67658	Human PRO
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14.27	1427.4	47.3	1429	8	ADB85961	Novel hum
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14.29	1427.4	47.3	1429	8	ADA97173	Human PRO
14.30	1427.4	47.3	1429	8	ADA79477	Human PRO
14.31	1427.4	47.3	1429	8	ADA87616	Novel hum
14.32	1427.4	47.3	1429	8	ADB16818	Human PRO
14.33	1427.4	47.3	1429	8	ADA91910	Novel hum
14.34	1427.4	47.3	1429	8	ADB14973	Human PRO
14.35	1427.4	47.3	1429	8	ADB18934	Novel hum
14.36	1427.4	47.3	1429	8	ADA94149	Human PRO
14.37	1427.4	47.3	1429	8	ADB20045	Novel hum

ALIGNMENTS

RESULT 1	
XX	AAAF29360
XX	AAAF29360 standard; DNA; 3017 BP.
XX	PAC
XX	AAF29360;
XX	20-APR-2001 (first entry)
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XX	Amlyoid-beta protein agglutination regulating factor DNA SEQ ID 7.
XX	Human; amlyoid-beta protein; agglutination regulatory factor;
XX	Alzheimer's disease; ds.
XX	
XX	Homo sapiens.
XX	
XX	WO200104299-A1.
XX	
XX	18-JAN-2001.
XX	
XX	06-JUL-2000; 2000WC-JP004515.
XX	
XX	08-JUL-1999; 99JP-00194179.
XX	18-OCT-1999; 99US-0159586P.
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XX	(HELI-) HELIX RES INST.
XX	

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Qy	661	TAGAGAGGTCAACCAAAAGGAGTAAGCTGTAGCTCCAGAGACCTGAGTGAAAACA	720
Db	661	TAGAGAGGTCAACCAAAAGGAGTAAGCTGTAGCTCCAGAGACCTGAGTGAAAACA	720
Qy	721	AGACCAAGACAGACAGAGCTCCAGAGCCTCAGTGAGCGCTCAGCCAGCGCTGAGGCGACAG	780
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Qy	761	GCTGCGACACAGAGTSCCAGAGGAGGAGAGCTGCTTGCTACAGCAAGTCC	840
Db	761	GCTGCCACACAGAGTSCCAGAGGAGGAGAGCTGCTTGCTACAGCAAGTCC	840
Qy	841	AGACACAGCCCGATGCCAGTGTCCAGTGTGATTCMAAGAGCAAGTTGAGAAAGG	900
Db	841	AGACACAGCCCGATGCCAGTGTCCAGTGTGATTCMAAGAGCAAGTTGAGAAAGG	900
Qy	901	AAACCAATGAGATCCAGTGGTGAATGAGAGGCTCAGAGGAGCAGGCTGCGCGAGAGC	960
Db	901	AAACCAATGAGATCCAGTGGTGAATGAGAGGCTCAGAGGAGCAGGCTGCGCGAGAGC	960
Qy	961	CAGCGGGAGCAGAGTGGTGGAGACAGAGCTGTAGGTGGAGAGGCTTCGGGGGAGCGG	1020
Db	961	CAGCGGGAGCAGAGTGGTGGAGACAGAGCTGTAGGTGGAGAGGCTTCGGGGGAGCGG	1020
Qy	1021	GAGACTGGCGCAGACCCACAGCTGCAGGCTGCCCTGTCACTGAGCGCAGGAATCCAG	1080
Db	1021	GAGACTGGCGCAGACCCACAGCTGCAGGCTGCCCTGTCACTGAGCGCAGGAATCCAG	1080
Qy	1081	AGATGAGGGCCCTGAGCGAGACCAAGCTGTCAATCCCGAGCGGACAGGAGGAGCAGG	1140
Db	1081	AGATGAGGGCCCTGAGCGAGACCAAGCTGTCAATCCCGAGCGGACAGGAGGAGCAGG	1140
Qy	1141	AGCTGCCGGGAGGAGGAGAACCAAGCAAGCTGAGAGGAGAGTGACTACACATGG	1200
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Qy	1201	ATGAAATGACAGCAAGTCTGACAGACAGCAAGCAGCCCTGGCAGGAGATGACAGAA	1260
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Qy	1261	ACATAGATGTTTTAATGTTGAGATCAGAAAGAGACACCAATTAATTTACTTGATCAGC	1320
Db	1261	ACATAGATGTTTTAATGTTGAGATCAGAAAGAGACACCAATTAATTTACTTGATCAGC	1320
Qy	1321	GTGAAAGGGAGATCATACACTCTGAAATGAACTGGAAATCATATTTACACACAGGGCC	1380
Db	1321	GTGAAAGGGAGATCATACACTCTGAAATGAACTGGAAATCATATTTACACACAGGGCC	1380
Qy	1381	GAGAGATGACTTTAAATGTTCAAGGAGCTGAATGAACTGTGAAATGTGAATGTACTA	1440
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DB	1501	AAAAAGGAAATGGTCTTTTAAACAGCTTTTGGGGGGTACTTTGGAAAGTGTCTTAACAAAGGTG	1560
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DB	1561	TCACAATTTTTGGTAGTAGTATTTCTGTGAGAAGCTCAACACACAAAACCTGGAACATAGTT	1620
QY	1621	CTCCTTCAAGTGTGGGAGACAGCGGGGCTTCTGATCTGGAAATATACTTTGTGTAAAT	1680
DB	1621	CTCCTTCAAGTGTGGGAGACAGCGGGGCTTCTGATCTGGAAATATACTTTGTGTAAAT	1680
QY	1681	TAAACGCCACTATAGAAAGTCCATCTGCTGTGAAGGAGACAGAGAACTCTGGGCTC	1740
DB	1681	TAAACGCCACTATAGAAAGTCCATCTGCTGTGAAGGAGACAGAGAACTCTGGGCTC	1740
QY	1741	CGTGTCTCTCCAGTGTGTGTACCAAGTGTGTGTGGGAGGCTGTACCTGTGTCTACTG	1800
DB	1741	CGTGTCTCTCTCCAGTGTGTGTACCAAGTGTGTGTGGGAGGCTGTACCTGTGTCTACTG	1800
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QY	1861	GCTTAGGACTGACTGTGTAAACAGAGCTGACTAGCAAGTAGCAAGAGTGTAAAGTCT	1920
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QY	1921	AAATCAAGAGTGTCTGTGTGAAGATTTTTTAAAGGCTACTTGTATATAACCGTTGT	1980
DB	1921	AAATCAAGAGTGTCTGTGTGAAGATTTTTTAAAGGCTACTTGTATATAACCGTTGT	1980
QY	1981	CATTTTTAATGTACAAAACGCTATTAAGTGGCTTGAATTTGAACATTTGTGTCTTTAT	2040
DB	1981	CATTTTTAATGTACAAAACGCTATTAAGTGGCTTGAATTTGAACATTTGTGTCTTTAT	2040
QY	2041	TTACTTGTTCGTGTGTGGCAAGCAACAATCTCCCTTAATATATATATACCGAGAAA	2100
DB	2041	TTACTTGTTCGTGTGTGGCAAGCAACAATCTCCCTTAATATATATATACCGAGAAA	2100
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DB	2161	AGAGCATGCTGAGAGGCAAGGCATGAGAGGGCAAGTTTTTGTGTGGACAGATCTGTGCT	2220
QY	2221	ACTTTATCTGAGTGTAAAGAAACAAAGTTGATGTGCGAGGATATATACAGTGT	2280
DB	2221	ACTTTATCTGAGTGTAAAGAAACAAAGTTGATGTGCGAGGATATATACAGTGT	2280
QY	2281	TAGAATATAGACTGTTTAGAAAAACAGAAATACATGTTTGTATCATAGTGTACA	2340
DB	2281	TAGAATATAGACTGTTTAGAAAAACAGAAATACATGTTTGTATCATAGTGTACA	2340
QY	2341	CATTTAGCTTGTGTAAATGACTCACAAAACCTGATTTTAAATCAAGTTTAATGTGATTT	2400
DB	2341	CATTTAGCTTGTGTAAATGACTCACAAAACCTGATTTTAAATCAAGTTTAATGTGATTT	2400
QY	2401	TGAATATACTACTTAATCCTAATTCAGATACAAATGGCATTTAGGTTTGACTTGAGTT	2460
DB	2401	TGAATATACTACTTAATCCTAATTCAGATACAAATGGCATTTAGGTTTGACTTGAGTT	2460

08-JUL-1999; 99JP-00194;79.
11-JAN-2000; 2000JP-00118775.
02-MAY-2000; 2000JP-00183766.
(HELI-) HELIX RES INST.
Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;
WPI; 2001-093989/11.
P-PDS; AAB88480.
Nucleic acids encoding secretory proteins/membrane proteins, useful in
gene therapy or as candidate target molecules in drug development.
Claim 1; SEQ ID NO 327; 609bp + Sequence Listing; English.
This invention relates to nucleic acid sequences AAF93744 - AAF93916
which encode human secretory or membrane proteins represented by AAB98317
- AAB88419. Invention in the invention are primers AAF93917 - AAF94295 and
AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the
invention. The invention also includes methods for the production of
antibodies directed against the proteins, and cDNA sequences, which can
be used in vaccines. The polynucleotide sequences can be used in gene
therapy. The polynucleotide sequences and the proteins they encode may be
used in the prevention, treatment and diagnosis of diseases associated
with inappropriate secretory protein/membrane protein expression. The
nucleic acids and complementary sequences may also be used as DNA probes
in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect
and quantitate the presence of similar nucleic acid sequences in samples.
They may also be used to study the expression and function of secretory
proteins/membrane polypeptides and their role in metabolism. The
polypeptides may be used as antigens in the production of antibodies
against them and in assays to identify modulators (agonists and
antagonists) of expression and activity. The antibodies and antagonists
may also be used as therapeutic agents to down regulate expression and
activity. The antibodies may also be used as diagnostic agents for
detecting the presence of the polypeptides in samples (e.g. by enzyme
linked immunosorbent assay (ELISA)). Examples of diseases which may be
treated include rheumatoid arthritis and diabetes

Query Match 100.0%; Score 3017; DB 5; Length 3017;

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 3017; Conservative 0; Mismatches 0; Indels 0;
```

1 GCTTGGGGCA CGGCG CGGAGGCCGGGGAGCTTGGAGGCCGGGGCGGCGGAGAGCGACC 60

1 GCTGGGCGCA CGGCGCGGA GCCGGCCGA GCTCGAGGCCGGCGCGCGGAGAGCGACC 60

61 CGGGGGCTT CGTAGGGGGCCCGGATCCCGAGTGGCGGCGGAGCCTCGAAGAAGA 120

61 CGGCGGGCCTCGTAGGGGGCCCGGATCCCGAGTGGCGGCCGAGCCTCGAAGAAGA 120

121 TTCTCAGCGCTGATTTT GAGATGATCGGCTTGGGAAAGGGGGCTCGCAGCATGAAGTCGC 180

121 TTCTCAGCGCTGATTTTGAGATGATGGCTTGGGACGGGGCTGCACCATGAATCGC 180

181 OGGCCCTCGTGTCTGGCCGCCCTGGTGGCCTGCATCATGGTCTTGGGCTCAACTACTGGA 240

181 CGCGCCTCGTGTGGCGGCGCTGGTGGCCGTGCAATCATGTCCTTGGGCTTCAACTACTGGA 240

241 TTGGAGCTCCGGAGGTGGACCTCCAGACACGGATCATGGAGCTGGAGGACAGGGTC 300

Db 241 TTGCGAGTCCCGGAGCGTGGAGCTCCAGACAGCGATCATGAGCTGGAGGCGAGGTCC 300
Qy 301 GCAGGCGGCTGCAGAGAGAGCGCGCTGAGCTGAAAGAAACGAGTTCCAGGAGAGCG 360
Db 301 GCAGGCGGCTGCAGAGAGAGCGCGCTGAGCTGAGAGAAACGAGTTCCAGGAGAGCG 360
Qy 361 TGGAGAAAGAGCGGAGAGAGCTTGAACAAATCGAGTCCAGGCCACATCTCCAGCTGGAGA 420
Db 361 TGGAGAGAGAGCGGAGAGAGCTTGAACAAATCGAGTCCAGGCCACATCTCCAGCTGGAGA 420
Qy 421 GCGTCAACAGAGCTACCAAGAGCGAAGAGGCGGTTTGGTGAATAACATCACACAGGTG 480
Db 421 GCGTCAACAGAGCTACCAAGAGCGAAGAGGCGGTTTGGTGAATAACATCACACAGGTG 480
Qy 481 AGAGGCTCATCCAGAGTGCACAGAGAGAGTTAAAGACCGCTGCAGAGGAATACGCGAGGC 540
Db 481 AGAGGCTCATCCAGAGTGCACAGAGAGAGTTAAAGACCGCTGCAGAGGAATACGCGAGGC 540
Qy 541 TGCAGAGAGATGTCCTCCAGTTTCAAGAGAGAGAGAGAGAGCTTGAAGAGAGTTCCTCT 600
Db 541 TGCAGAGAGATGTCCTCCAGTTTCAAGAGAGAGAGAGAGAGCTTGAAGAGAGTTCCTCT 600
Qy 601 ACGAGCTGAGCGAGTGCATCAATCAGATGAAGAGAGTGAAGAACAGTGTGAGAGAGCGAA 660
Db 601 ACGAGCTGAGCGAGTGCATCAATCAGATGAAGAGAGTGAAGAACAGTGTGAGAGAGCGAA 660
Qy 661 TAGAAGAGGTCAACAAAAGGAGATGAAGCTGTAGCTTCCAGAGAGAGCTGAGTGAAGAAC 720
Db 661 TAGAAGAGGTCAACAAAAGGAGATGAAGCTGTAGCTTCCAGAGAGAGCTGAGTGAAGAAC 720
Qy 721 ACGAGCAGAGAGAGAGCTCCAGAGCTTCAGTGAAGCTCAGGCCAGAGAGAGAGAG 780
Db 721 ACGAGCAGAGAGAGAGCTCCAGAGCTTCAGTGAAGCTCAGGCCAGAGAGAGAGAGAG 780
Qy 781 GCGTGCACACAGAGAGTGCACAGGAGAGGAGAGAGAGTGTGTTAAACAGCAAGTCCC 840
Db 781 GCGTGCACACAGAGAGTGCACAGGAGAGGAGAGAGAGTGTGTTAAACAGCAAGTCCC 840
Qy 841 AGACACAGCCCCCAGTTCGGAAGTGGTTTGGATTCAAGAGAGAGAGTGGAGAGAGAG 900
Db 841 AGACACAGCCCCCAGTTCGGAAGTGGTTTGGATTCAAGAGAGAGAGTGGAGAGAGAG 900
Qy 901 AAACCAATGAGTCCAGTGGTGAATGAGAGAGAGAGAGAGAGAGTGCAGAGAGAGAG 960
Db 901 AAACCAATGAGTCCAGTGGTGAATGAGAGAGAGAGAGAGAGAGTGCAGAGAGAGAG 960
Qy 961 CAGGCGGAGAGAGAGTGTGAGAGAGAGAGAGAGAGAGTGTGAGAGAGAGAGAGAGAG 1020
Db 961 CAGGCGGAGAGAGAGTGTGAGAGAGAGAGAGAGAGAGTGTGAGAGAGAGAGAGAGAG 1020
Qy 1021 GAGAGTGGGCGAG 1080
Db 1021 GAGAGTGGGCGAG 1080
Qy 1081 AGATGAG 1140
Db 1081 AGATGAG 1140
Qy 1141 AAGCTGCCGCGAG 1200
Db 1141 AAGCTGCCGCGAG 1200

Qy 1201 ATGAAGATGAAGAGAGATCTGAGACAGACAAAGCAAGAGAGAGAGAGAGAGAGAGAG 1260
Db 1201 ATGAAGATGAAGAGAGATCTGAGACAGACAAAGCAAGAGAGAGAGAGAGAGAGAGAG 1260
Qy 1261 ACATAGAGTGTTTTAATGTTGAAGATCAGAAAAGAGAGACCAATAAATTTACTTGTGACG 1320
Db 1261 ACATAGAGTGTTTTAATGTTGAAGATCAGAAAAGAGAGACCAATAAATTTACTTGTGACG 1320
Qy 1321 GTGAAGAGGAGATCATACACTCTGAATGAACTGGAATCACATATTTCAACACAGGGCC 1380
Db 1321 GTGAAGAGGAGATCATACACTCTGAATGAACTGGAATCACATATTTCAACACAGGGCC 1380
Qy 1381 GAAAGATGACTTTAAATGTTTCAATGAGGAGCTGAATGACTGAAAAGCTGTGAATTTACTA 1440
Db 1381 GAAAGATGACTTTAAATGTTTCAATGAGGAGCTGAATGACTGAAAAGCTGTGAATTTACTA 1440
Qy 1441 AATAAATGTACATCTGAAGATGATATTTGAAAATTTTATATGACACTTTGTAGAGAA 1500
Db 1441 AATAAATGTACATCTGAAGATGATATTTGAAAATTTTATATGACACTTTGTAGAGAA 1500
Qy 1501 AAATGGAATGCTTTTAAACAGCTTTTGGGGGTACTTTGGAAGTGTCTATTAAGGTG 1560
Db 1501 AAATGGAATGCTTTTAAACAGCTTTTGGGGGTACTTTGGAAGTGTCTATTAAGGTG 1560
Qy 1561 TCACAATTTTGGTAGTAGTATTGTTGAGAGAGCTCAACACCAAAAGCTGGAACATAGTT 1620
Db 1561 TCACAATTTTGGTAGTAGTATTGTTGAGAGAGCTCAACACCAAAAGCTGGAACATAGTT 1620
Qy 1621 CTCCTCAAGTGTGGCAG 1680
Db 1621 CTCCTCAAGTGTGGCAG 1680
Qy 1681 TAAAGTGTGGTGTGAGAGAGTCCATCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
Db 1681 TAAAGTGTGGTGTGAGAGAGTCCATCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
Qy 1741 GGTCTCTCTGTCCAGAGTGTGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
Db 1741 GGTCTCTCTGTCCAGAGTGTGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
Qy 1801 AAAGTGTGGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAG 1860
Db 1801 AAAGTGTGGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAG 1860
Qy 1861 GGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 1920
Db 1861 GGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 1920
Qy 1921 AAATACAAAGCTGTCTGTGTGAGAGATTTTAAAGGCTACTTGTATATAACCCCTGT 1980
Db 1921 AAATACAAAGCTGTCTGTGTGAGAGATTTTAAAGGCTACTTGTATATAACCCCTGT 1980
Qy 1981 CATTTTAAAGTACAAAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 2040
Db 1981 CATTTTAAAGTACAAAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 2040
Qy 2041 TTAATTTGCTGTGTGGGCAAGCAACATCTTCCCTAAATATATATTAACCAAGAAA 2100
Db 2041 TTAATTTGCTGTGTGGGCAAGCAACATCTTCCCTAAATATATATTAACCAAGAAA 2100
Qy 2101 GGAAGAGAGAGATGTTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2160
Db 2101 GGAAGAGAGAGATGTTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2160
Qy 2161 GGAAGAGAGATGTTTGTGAG 2220
Db 2161 GGAAGAGAGATGTTTGTGAG 2220

QY 2161 AGAGCATGGTGGAGGCAAGGCGATGAGAGGCGAAGTTTGTGTGGACAGATCTGTGCTT 2220
 DB |||||||
 QY 2161 AGAGCATGGTGGAGGCAAGGCGATGAGAGGCGAAGTTTGTGTGGACAGATCTGTGCTT 2220
 DB |||||||
 QY 2221 ACTTTATCTGGAGTAAAGAAACAAAGTTCATTTGATGTCGAGGATATATACAGTGT 2280
 DB |||||||
 QY 2221 ACTTTATCTGGAGTAAAGAAACAAAGTTCATTTGATGTCGAGGATATATACAGTGT 2280
 DB |||||||
 QY 2281 TAGAATATAGGCTGTGTAGAAAACAGGAATACAAATGGTTTGTATCATAGTGTACA 2340
 DB |||||||
 QY 2281 TAGAATATAGGCTGTGTAGAAAACAGGAATACAAATGGTTTGTATCATAGTGTACA 2340
 DB |||||||
 QY 2341 CATTTAGCTTGTGTAAATGACTCACAAAACAGTAAATCAATCAATGATGATGATTT 2400
 DB |||||||
 QY 2341 CATTTAGCTTGTGTAAATGACTCACAAAACAGTAAATCAATCAATGATGATGATTT 2400
 DB |||||||
 QY 2401 TGAATATCTACTTAATCTCAATTCACAAATGAGCTTAAGGTTTGTGACTTGTAGTT 2460
 DB |||||||
 QY 2401 TGAATATCTACTTAATCTCAATTCACAAATGAGCTTAAGGTTTGTGACTTGTAGTT 2460
 DB |||||||
 QY 2461 GGTCTTGTATTTATTTTGGTAAATAGGCTCTTACCACTTGCATTAATGCTGCGCACATC 2520
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 QY 2461 GGTCTTGTATTTATTTTGGTAAATAGGCTCTTACCACTTGCATTAATGCTGCGCACATC 2520
 DB |||||||
 QY 2521 ATTAAATGACTGACTTCCAGATAGGCTCTTAAAGGGTAAAGTGAAGGATCCACAGATTT 2580
 DB |||||||
 QY 2521 ATTAAATGACTGACTTCCAGATAGGCTCTTAAAGGGTAAAGTGAAGGATCCACAGATTT 2580
 DB |||||||
 QY 2581 TGAGATGCTTAAGGCGCCAGAGATGTTTGAACCAACCTCTTATTTTCAGAGGCGAAAT 2640
 DB |||||||
 QY 2581 TGAGATGCTTAAGGCGCCAGAGATGTTTGAACCAACCTCTTATTTTCAGAGGCGAAAT 2640
 DB |||||||
 QY 2641 GGGGCTAGAGTTAGAGGATCTAGCTGGTGGTGGCGACCCCTGGCTCACACAGAC 2700
 DB |||||||
 QY 2641 GGGGCTAGAGTTAGAGGATCTAGCTGGTGGTGGCGACCCCTGGCTCACACAGAC 2700
 DB |||||||
 QY 2701 TCCGAGTGTGGGACTACAGGACACAGTCACTGAAGCAGGCGCCCTGTTGCAATTCAC 2760
 DB |||||||
 QY 2701 TCCGAGTGTGGGACTACAGGACACAGTCACTGAAGCAGGCGCCCTGTTGCAATTCAC 2760
 DB |||||||
 QY 2761 GCTGCCACTCCAACTTAACATTTCTCATATGATGTCCTTAGTCACTAAGGTTAAAC 2820
 DB |||||||
 QY 2761 GCTGCCACTCCAACTTAACATTTCTCATATGATGTCCTTAGTCACTAAGGTTAAAC 2820
 DB |||||||
 QY 2821 TTTCCACCCAGAAAAGGCACTTAGATAAAATCTTAGAGTACTTTCATCTCTTAAG 2880
 DB |||||||
 QY 2821 TTTCCACCCAGAAAAGGCACTTAGATAAAATCTTAGAGTACTTTCATCTCTTAAG 2880
 DB |||||||
 QY 2881 TCCCTCTCCAGCCTCACTTTGAGTCCCTCTTGGGTTGATAGGATTTTCTCTGCTTC 2940
 DB |||||||
 QY 2881 TCCCTCTCCAGCCTCACTTTGAGTCCCTCTTGGGTTGATAGGATTTTCTCTGCTTC 2940
 DB |||||||
 QY 2941 TCAATAAGTCTCTATTCACTCTCATGTTTAAATTTAGGCAATGAGATTTGCTGAGAAATA 3000
 DB |||||||
 QY 2941 TCAATAAGTCTCTATTCACTCTCATGTTTAAATTTAGGCAATGAGATTTGCTGAGAAATA 3000
 DB |||||||
 QY 3001 AATGTTCTGTCAACTT 3017
 DB |||||||
 QY 3001 AATGTTCTGTCAACTT 3017
 DB |||||||

RESULT 3

AAC64559
 ID AAC64559 standard; cDNA; 3051 BP.
 XX
 AC AAC64559;
 XX
 DT 14-FEB-2001 (first entry)
 XX
 DE Human prostate specific gene 30P3C8 nucleotide sequence SEQ ID NO:1.
 XX
 KW Human; prostate specific gene; 30P3C8; prostate cancer; diagnosis;
 KW cytostatic; gene therapy; vaccine; tumour; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200061610-R2.
 XX
 PD 19-OCT-2000.
 XX
 XX 12-APR-2000; 2000WO-US010218.
 PF
 XX 12-APR-1999; 99US-0128660P.
 PR
 XX (UROC-) UROGENESYS INC.
 PA
 PI Afar DE, Hubert RS, Leong K, Raitano AB, Saffran DC;
 XX
 XX WPI: 2000-619224/59.
 DR
 DR P-PSDB; A0524352.
 XX
 XX 30P3C8 polypeptide and polynucleotide used for diagnosing, treating and
 PT monitoring development of prostate cancer.
 FT
 PS Claim 1; Page 92-94; 99pp; English.
 XX
 XX The present sequence encodes the human prostate specific protein 30P3C8,
 CC which is over-expressed in prostate cancer cells. 30P3C8 has cytostatic
 CC activity and can be used in vaccines and gene therapy. Methods for
 CC detecting the levels of 30P3C8 protein or mRNA in prostate tissue, bone
 CC tissue, lymphatic tissue, serum, blood or semen are used for diagnosing
 CC the presence of cancer in an individual or dysregulated cell growth e.g.
 CC hyperplasia. The cancers which are detected or diagnosed are of the
 CC bladder, pancreas, colon, brain, bone, lung, kidney or prostate by using
 CC test samples of serum, blood or urine or tissues of the bladder,
 CC pancreas, colon, brain, bone, lung, kidney and prostate. 30P3C8
 CC polynucleotide sequences can be used for treating cancers expressing
 CC 30P3C8, particularly prostate cancers. Immunogenic portions of 30P3C8 are
 CC used in vaccines to inhibit the development of cancer. Anti-30P3C8
 CC monoclonal antibodies bind to 30P3C8 and disrupt interactions between
 CC 30P3C8 and other proteins e.g. receptors for which 30P3C8 is a ligand.
 CC 30P3C8 may be a growth factor or other molecule involved in tumour growth
 CC and metastasis and so anti-30P3C8 antibodies may disrupt the homing or
 CC invasion or other cancer promoting activities of 30P3C8. The assays are
 CC used for detecting, staging and monitoring prostate cancer. The 30P3C8
 CC protein or mRNA are used as additional specific markers for detecting
 CC prostate cancer and provide a more specific assay than the serum prostate
 CC specific antigen (PSA) assay
 XX
 SQ Sequence 3051 BP; 909 A; 638 C; 808 G; 696 T; 0 U; 0 Other;
 Query Match 99.4%; Score 2998.6; DB 3; Length 3051;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 3012; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY	1	GTCTGAGGCGCATGGGCGCGAGAGCCGCGAGCTCGAGCGCGGCGGCGGAGCGAGCC	60
DB	20	GCTGAGCGCATGCGCGCGAGCGCGCGGAGCTGAGAGCGCGCGCGCGGCGGAGCGAGCC	79
QY	61	CGGCGGCGCTGCTAGCGGCGCGCGGATCCCGAGTGCCTCGAGTGGCGGCGGAGAGCTCGAAAAGAGA	120
DB	80	CGGCGGCGCTGCTAGCGGCGCGCGGATCCCGGATCCCGGCTGGCGGCGGAGGCTCGAAAAGAGA	139
QY	121	TTCTCAGCGGCTGATTTTGAGATGATGGGCTTGGGAAAGCGGCGTGCAGCATGAGTGGC	180
DB	140	TTCTCAGCGGCTGATTTTGAGATGATGGGCTTGGGAAAGCGGCGTGCAGCATGAGTGGC	199
QY	181	GGCGGCTGGTGGTGGCGCGCTGGTGGCGCTGCATCATGGTCTTGGGCTTCAACTCTCGA	240
DB	200	GGCGGCTGGTGGTGGCGCGCTGGTGGCGCTGCATCATGGTCTTGGGCTTCAACTCTCGA	259
QY	241	TTGGCGAGCTCCCGAGCGGCTGAGCTCCAGACACGCGATCATGAGCTGGAAAGCGAGGCTCC	300
DB	260	TTGGCGAGCTCCCGAGCGGCTGAGCTCCAGACACGCGATCATGAGCTGGAAAGCGAGGCTCC	319
QY	301	GCAAGCGGCTTCAGAGAGAGGCGCGTGGAGCTGAAGAAGAAAGAGTTTCCAGGGAGAGC	360
DB	320	GCAAGCGGCTTCAGAGAGAGGCGCGTGGAGCTGAAGAAGAAAGAGTTTCCAGGGAGAGC	379
QY	361	TGGAGAAACAGCGGGAGCGAGCTTGACAAATCCAGTCCAGGCCACACTTCCAGCTGGA	420
DB	380	TGGAGAAACAGCGGGAGCGAGCTTGACAAATCCAGTCCAGGCCACACTTCCAGCTGGA	439
QY	421	GGGTCAACAGCTGTACCGAGCGAAAGCGGTTTGGTGATTAACATCACACACAGGTCG	480
DB	440	GGGTCAACAGCTGTACCGAGCGAAAGCGGTTTGGTGATTAACATCACACAGGTCG	499
QY	481	AGAAGCTCATCCGAGTCTGCAAGACAGTTTAAAGACCCCTGCAGAGAAATTACCGGAGCG	540
DB	500	AGAAGCTCATCCGAGTCTGCAAGACAGTTTAAAGACCCCTGCAGAGAAATTACCGGAGCG	559
QY	541	TGCAGCAGGATGCTCTCAGGTTTCAGAGAAACAGACCAACCTGGAAGAGGATCTCTCT	600
DB	560	TGCAGCAGGATGCTCTCAGGTTTCAGAGAAACAGACCAACCTGGAAGAGGATCTCTCT	619
QY	601	ACGAGCTGAGCCAGTGCATCATAGATGAAGAGTGAAGGAACAGTGTGAGGAGCGAA	660
DB	620	ACGAGCTGAGCCAGTGCATCATAGATGAAGAGTGAAGGAACAGTGTGAGGAGCGAA	679
QY	661	TAGAAGAGTCAACCAAAAAGGGAATGAAGCTGTAGCTTCAGAGACCTGAGTGAANA	720
DB	680	TAGAAGAGTCAACCAAAAAGGGAATGAAGCTGTAGCTTCAGAGACCTGAGTGAANA	739
QY	721	ACGACCAAGACAGACAGCGCTCCAGGCTCAGCGCTCAGCGCTCAGAGCGACGAG	780
DB	740	ACGACCAAGACAGACAGCGCTCCAGGCTCAGCGCTCAGCGCTCAGAGCGACGAG	799
QY	781	GCTTGGCAGCAGCAGAGTGCACAGAGGAAGGAAGCTGCTTGGTAAACAGCAAGTCC	840
DB	800	GCTTGGCAGCAGCAGAGTGCACAGAGGAAGGAAGCTGCTTGGTAAACAGCAAGTCC	859
QY	841	AGACACAGCGCCCGAGTTCGGAAGTGGTTTGGATTCAAAGAGACAAGTTTGAAAGAGG	900
DB	860	AGACACAGCGCCCGAGTTCGGAAGTGGTTTGGATTCAAAGAGACAAGTTTGAAAGAGG	919
QY	901	AAACCAATGAGATCCAGTGGTGAATGAGAGCGCTCAGAGGAGCAGGCTGCGCGAGAGC	960
DB	920	AAACCAATGAGATCCAGTGGTGAATGAGAGCGCTCAGAGGAGCAGGCTGCGCGAGAGC	979

QY	961	CAGGCCGGGAGCGAGTGGTGGAGACAGACTGTGTAGTTGGAGAGAGGCTTCGGGGGAGCGC	1020
Ds	980	CAGGCCGGGAGCGAGTGGTGGAGACAGCACTGGTGGTGGAGAGAGGCTTCGGGGGAGCGC	1039
QY	1021	GAGAAGCTGGGCGCACCCGCACAGGTCAGAGCTGGCCCTGTCACTGAGAGCGAGAAAATCCAG	1080
Ds	1040	GAGAACTGGGCGCAGACCOCACAGGTCAGAGCTGGCCCTGTCACTGAGCGAGAAAATCCAG	1099
QY	1081	AGATGGAGGGCCCTGAGCGAGACGAGCTTTGATCCOOCACGGACAGGAGGAGGACGAGG	1140
Ds	1100	AGATGGAGGGCCCTGAGCGAGACGAGCTTTGATCCOOCACGGACAGGAGGAGGAGGACGAGG	1159
QY	1141	AAGCTCCGGGGAGGGGAGAAAAACGACAGAAAATGAGGAGGAACAAGTACTACACATGG	1200
Ds	1160	AAGCTCCGGGGAGGGGAGAAAAACGACAGAAAATGAGGAGGAACAAGTACTACACATGG	1219
QY	1201	ATGAAAATGAAGCAGAAATCTGACAGACAAAGCAGACAGCCCTGGCAGGGAATACAGAA	1260
Ds	1220	ATGAAAATGAAGCAGAAATCTGACAGACAAAGCAGACAGCCCTGGCAGGGAATACAGAA	1279
QY	1261	ACATAGATGTTTTAATGTTGAAGATCAGAAAAGAGACACATAAATTACTTGATCAGC	1320
Ds	1280	ACATAGATGTTTTAATGTTGAAGATCAGAAAAGAGACACATAAATTACTTGATCAGC	1339
QY	1321	GTGAAAAGCGGAATCATACACTGTGAATGGAATGGMAIACACATMTTCACACAGGGCC	1380
Ds	1340	GTGAAAAGCGGAATCATACACTGTGAATGGAATGGMAIACACATMTTCACACAGGGCC	1399
QY	1381	GACAGATGACTTTAAATGTTGATGAGGACCTGAATACTGAAAACCTGTGAATGTACTA	1440
Ds	1400	GACAGATGACTTTAAATGTTGATGAGGACCTGAATACTGAAAACCTGTGAATGTACTA	1459
QY	1441	AATAAAAATGATCTGAAGATGATTTATTTGMAATTTTAGTAIGCACTTTGTGAGAA	1500
Ds	1460	AATAAAAATGATCTGAAGATGATTTATTTGMAATTTTAGTAIGCACTTTGTGAGAA	1519
QY	1501	AAAAATGGAATGGTCTTTAAACAGCTTTTGGGGGCTACTTTGSAAGTGTCTAATAAGGTG	1560
Ds	1520	AAAAATGGAATGGTCTTTAAACAGCTTTTGGGGGCTACTTTGSAAGTGTCTAATAAGGTG	1579
QY	1561	TACAAATTTTTGGTAGTAGTATTCGTGAGAGCTCAACACAAAACTGGMACATAGTT	1620
Ds	1580	TACAAATTTTTGGTAGTAGTATTCGTGAGAGCTCAACACAAAACTGGMACATAGTT	1639
QY	1621	CTCCTTCAGTGTGGGACAGCGGGGCTTCCTGATTCGGAATATACTTTGTGTAAT	1680
Ds	1640	CTCCTTCAGTGTGGGACAGCGGGGCTTCCTGATTCGGAATATACTTTGTGTAAT	1699
QY	1681	TAAACGCCACTATAGAGAGTCCATCTGCTGTAAGGAGACAGAGAACTCTGGGTTTC	1740
Ds	1700	TAAACGCCACTATAGAGAGTCCATCTGCTGTAAGGAGACAGAGAACTCTGGGTTTC	1759
QY	1741	GCTGGTCTGTGCACGTGCTGTACCAAGTGGTGGTGGCGAGGCTGTTAACCTGTCTCACTG	1800
Ds	1760	GCTGGTCTGTGCACGTGCTGTACCAAGTGGTGGTGGCGAGGCTGTTAACCTGTCTCACTG	1819
QY	1801	AAAAAGTCTGGCTAAATGCTCTGTGTAGTCACCTCTGANTCTGCAATCAATCAATCAATG	1860
Ds	1820	AAAAAGTCTGGCTAAATGCTCTGTGTAGTCACCTCTGANTCTGCAATCAATCAATCAATG	1879
QY	1861	GCTTAGAGCACTGACTGTTAAACAAACGCTCACTAGCAAAGTAGCAAGCTTTAAGTCT	1920

Db 1880 GCTTAGAGCACTGACTGTTTAAACAAAGCTCACTAGCAAAAGTAGCAACAGCTTTAAGTCT 1939
QY 1921 AAATACAAAGCTGTTCTGTGTGAGAAATTTTAAAGGCTACTTGTATATAATACCCCTGT 1980
Db 1940 AAATACAAAGCTGTTCTGTGTGAGAAATTTTAAAGGCTACTTGTATATAATACCCCTGT 1999
QY 1981 CATTTTAAATGTACAAAGCGCTATTAAGTGGCTTAGAATTTGAACATTTTGGGCTTTAT 2040
Db 2000 CATTTTAAATGTACAAAGCGCTATTAAGTGGCTTAGAATTTGAACATTTTGGGCTTTAT 2059
QY 2041 TACTTTGCTTCTGTGTGGCAAGCAACATCTTCCCTAATATATATATACCAAGAAA 2100
Db 2060 TACTTTGCTTCTGTGTGGCAAGCAACATCTTCCCTAATATATATATACCAAGAAA 2119
QY 2101 GCAAGACGAGATTAGGTTTTTGAACAAACAAACAGGCCAAAAGGGGGCTGACCTGGAGC 2160
Db 2120 GCAAGACGAGATTAGGTTTTTGAACAAACAAACAGGCCAAAAGGGGGCTGACCTGGAGC 2179
QY 2161 AGAGCATGGTGAGGCAAGCGCATGAGAGGCGAAGTTTTGTGTGGACAGATCTGTGGCT 2220
Db 2180 AGAGCATGGTGAGGCAAGCGCATGAGAGGCGAAGTTTTGTGTGGACAGATCTGTGGCT 2238
QY 2221 ACTTTAATGAGTAAAGAAACAAACAAAGTTCAATTCATGTCGAAGGATATATACAGTGT 2280
Db 2239 ACTTTAATGAGTAAAGAAACAAACAAAGTTCAATTCATGTCGAAGGATATATACAGTGT 2298
QY 2281 TAGAATTAGGATGTTTGAACAAACAAACAGGAATACATGGTGTTTTATCATAGTGACA 2340
Db 2299 TAGAATTAGGATGTTTGAACAAACAAACAGGAATACATGGTGTTTTATCATAGTGACA 2358
QY 2341 CATTTAGCTGTGGTAAATGACTCACAAACATGATTTTAAATCAAGTTAATGTGAATTT 2400
Db 2359 CATTTAGCTGTGGTAAATGACTCACAAACATGATTTTAAATCAAGTTAATGTGAATTT 2418
QY 2401 TGAATATGACTGATTAATCCTAATCACAAATACAAATGGCATTAAAGTTTGGACTTGGTT 2460
Db 2419 TGAATATGACTGATTAATCCTAATCACAAATACAAATGGCATTAAAGTTTGGACTTGGTT 2478
QY 2461 GGTTCCTTAGTATTAATTTATGTAATAGGCTCTTACACATTCGAAATACCTGCCACATC 2520
Db 2479 GGTTCCTTAGTATTAATTTATGTAATAGGCTCTTACACATTCGAAATACCTGCCACATC 2538
QY 2521 ATTAATGACTGACTTCCAGTAAGGCTCTCTAAGGGTAAAGTAGGAGGATCCACAGGATT 2580
Db 2539 ATTAATGACTGACTTCCAGTAAGGCTCTCTAAGGGTAAAGTAGGAGGATCCACAGGATT 2598
QY 2581 TGAGATGCTAAGGCCCCAGAGATCGTTTGAACCAACCTCTTATTTTCAAGGGGAAAAAT 2640
Db 2599 TGAGATGCTAAGGCCCCAGAGATCGTTTGAACCAACCTCTTATTTTCAAGGGGAAAAAT 2658
QY 2641 GGGGCGCTAGAAGTTACAGAGCATCTAGCTGGTGGCGACCCCTGGGCTCACACAGAC 2700
Db 2659 GGGGCGCTAGAAGTTACAGAGCATCTAGCTGGTGGCGACCCCTGGGCTCACACAGAC 2718
QY 2701 TCCGAGTACTGGGACTACAGGACACAGTCACTGAAGCAGGGCCCTGTTGCAATTCAC 2760
Db 2719 TCCGAGTACTGGGACTACAGGACACAGTCACTGAAGCAGGGCCCTGTTGCAATTCAC 2778
QY 2761 GCTGCCACTCCAACTTAAACATCTTCAATGTGATGCTTAGTCACTAAGGTTAAAC 2820
Db 2779 GTTGCCACTCCAACTTAAACATCTTCAATGTGATGCTTAGTCACTAAGGTTAAAC 2838
QY 2821 TTTCGCCACCCAGAAAGGCACTTAGATAAATCTTAGAGTACTTTCTCTAAG 2880

Db 2839 TTTCGCCACCCAGAAAGGCACTTAGATAAATCTTAGAGTACTTTCTACTCTCTAAG 2898
QY 2881 TCCCTCTTCAGGCTCACTTTGAGTCCCTCTGGGTTGATAGGAATTTCTCTGCTTTC 2940
Db 2899 TCCCTCTTCAGGCTCACTTTGAGTCCCTCTGGGTTGATAGGAATTTCTCTGCTTTC 2958
QY 2941 TCAATAAAGTCTCTATTCATCTCATCTGTTAATTTGTACGATAGATTTCTGAGAATAA 3000
Db 2959 TCAATAAAGTCTCTATTCATCTCATCTGTTAATTTGTACGATAGATTTCTGAGAATAA 3018
QY 3001 AATGTTCTGTTCACCTT 3017
Db 3019 AATGTTCTGTTCACCTT 3035
RESULT 4
ID ABV25476 standard; cDNA; 3210 BP.
XX
AC ABV25476;
XX
16-SEP-2002 (first entry)
XX Human prostate expression marker cDNA 25467.
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX Homo sapiens.
XX WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US005171.
XX
XX 17-FEB-2000; 2000US-0183319P.
ER 16-MAR-2000; 2000US-0189622P.
ER 25-MAY-2000; 2000US-0207454P.
PR 09-JUN-2000; 2000US-0211314P.
PR 18-JUL-2000; 2000US-0219007P.
PR 13-DEC-2000; 2000US-0255281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Schlegel R, Endege WO, Monahan JE;
XX WPI; 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
prostate cells and correlating with presence of prostate cancer, useful
for detecting presence of prostate cancer, stage of prostate cancer.
XX
PS Claim 1; Page 5059-5060; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
specification or its complement. (I) is useful for: (a) assessing whether
a patient is afflicted with prostate cancer; (b) monitoring the
progression of prostate cancer in a patient; (c) assessing the efficacy
of a test compound to inhibit prostate cancer in a patient; (d) assessing
the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC

CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
 CC determining whether prostate cancer has metastasized in a patient; (h)
 CC assessing the aggressiveness or indolence of prostate cancer in a patient
 CC ; (i) is also useful as a pharmacodynamic or pharmacogenomic marker
 XX
 SQ Sequence 3210 BP; 926 A; 701 C; 856 G; 717 T; 0 U; 10 Other;

Query Match		99.4%	Score 2998.6;	DB 5;	Length 3210;
Best Local Similarity		99.8%	Pred. No. 0;		
Matches 3012;		Conservative	0;	Mismatches	4;
				Indels	1;
				Gaps	1;
QY	1	GCTGGCCGCAAGCGCGGAGCGCGGCGGAGCTGAGAGCTGAGAGCGCGGCGGCGGAGAGCGAGC	60		
DB	133	GCTGGCGCAAGCGCGGAGCGCGGCGGAGCTGAGAGCTGAGAGCGCGGCGGCGGAGAGCGAGC	192		
QY	61	CGGCGGCGCTGAGAGCGCGCGCGGATCCCGGAGTGGCGCGCGGAGCGCTCGGAGAGAGAG	120		
DB	193	CGGCGGCGCTGAGAGCGCGCGCGGATCCCGGAGTGGCGCGCGGAGCGCTCGGAGAGAGAG	252		
QY	121	TTCACGCGCTGATTTTGAGATGATGGGCTTGGGAAACGCGCGTGGCAGCATGAAGTCGC	180		
DB	253	TTCACGCGCTGATTTTGAGATGATGGGCTTGGGAAACGCGCGTGGCAGCATGAAGTCGC	312		
QY	181	CGGCGCTGCTGGCGCGCGCTGGTGGCTGGATCATCGCTTTGGGCTTCAACTACTGGA	240		
DB	313	CGGCGCTGCTGGCGCGCGCTGGTGGCTGGATCATCGCTTTGGGCTTCAACTACTGGA	372		
QY	241	TTCGAGCTCCCGGAGCGTGGAGCTCCAGAGCGGATCATGGAGCTGGAGGCGAGGCTCC	300		
DB	373	TTCGAGCTCCCGGAGCGTGGAGCTCCAGAGCGGATCATGGAGCTGGAGGCGAGGCTCC	432		
QY	301	GCAAGCGCGCTGCAGAGAGAGGCGCGCTGGAGCTGAAGAGAAACGAGTCCAGGGAGAGC	360		
DB	433	GCAAGCGCGCTGCAGAGAGAGGCGCGCTGGAGCTGAAGAGAAACGAGTCCAGGGAGAGC	492		
QY	361	TGAGAGAGAGCGCGGAGAGCTTGACAAATCCAGTCCAGCCACACCTTCCAGCTGGAGA	420		
DB	493	TGAGAGAGAGCGCGGAGAGCTTGACAAATCCAGTCCAGCCACACCTTCCAGCTGGAGA	552		
QY	421	GCTCAACAGCTGTACAGAGAGAAAGCGGCTTTGGTGAATTAACATCAACACAGGCTG	480		
DB	553	GCTCAACAGCTGTACAGAGAGAAAGCGGCTTTGGTGAATTAACATCAACACAGGCTG	612		
QY	481	AGAGGCTCATCCGAGTGTGCAAGAGCCAGTTAAGACCCCTGGCAGAGGATTAAGGAGGC	540		
DB	613	AGAGGCTCATCCGAGTGTGCAAGAGCCAGTTAAGACCCCTGGCAGAGGATTAAGGAGGC	672		
QY	541	TGACAGAGAGTGTCTCCAGCTTCAAGAGAAACGAGCCACCTGGAGGAGGATTCCTCT	600		
DB	673	TGACAGAGAGTGTCTCCAGCTTCAAGAGAAACGAGCCACCTGGAGGAGGATTCCTCT	732		
QY	601	ACGACCTGAGCGAGTGCATCAATCAGATGAAGAGGTTGAAGAGACAGTGTGAGAGAGGAA	660		
DB	733	ACGACCTGAGCGAGTGCATCAATCAGATGAAGAGGTTGAAGAGACAGTGTGAGAGAGGAA	792		
QY	661	TAGAGAGGTCAACCAAAAGGAGATGAAGCTGTAGCTTCCAGAGACCTGAGTGAAGACA	720		
DB	793	TAGAGAGGTCAACCAAAAGGAGATGAAGCTGTAGCTTCCAGAGACCTGAGTGAAGACA	852		
QY	721	ACGACAGAGAGAGAGCTCCAGGCGCTCAGTGAAGCTCAGGCGAGGCTGCAGGAGAG	780		
DB	853	ACGACAGAGAGAGAGCTCCAGGCGCTCAGTGAAGCTCAGGCGAGGCTGCAGGAGAG	912		

QY	781	GCTGGCCACACACAGAGGTCGACAGAGGAAAGGAAAGTGTCTTGGTACACAGCATCTCC	840
DB	913	GCTGGCCACACACAGAGGTCGACAGAGGAAAGGAAAGTGTCTTGGTACACAGCATCTCC	972
QY	841	AGACACACAGCCGCCAGTTCGAGAGTGTGGATCAAGAGACAAAGTTGAGAAAGAGG	900
DB	973	AGACACACAGCCGCCAGTTCGAGAGTGTGGATCAAGAGACAAAGTTGAGAAAGAGG	1032
QY	901	AAACCAATAGATCCAGTGGTGAAGAGACAGCTGTAGGTGGAAGAGGCTTCGCGGAGAGC	960
DB	1033	AAACCAATAGATCCAGTGGTGAAGAGACAGCTGTAGGTGGAAGAGGCTTCGCGGAGAGC	1092
QY	961	CAGCGCGGAGAGCTGGTGAAGAGACAGCTGTAGGTGGAAGAGGCTTCGCGGAGAGC	1020
DB	1093	CAGCGCGGAGAGCTGGTGAAGAGACAGCTGTAGGTGGAAGAGGCTTCGCGGAGAGC	1152
QY	1021	GAGAACTGGGCGCACCCACAGTTCAGAGCTGCTGTCACTGAGCCAGGAAATCCAG	1080
DB	1153	GAGAACTGGGCGCACCCACAGTTCAGAGCTGCTGTCACTGAGCCAGGAAATCCAG	1212
QY	1081	AGATGAGGCGGCTGAGGAGACAGCTGTCACTCCCGACGGAGACAGAGAGAGAGCAG	1140
DB	1213	AGATGAGGCGGCTGAGGAGACAGCTGTCACTCCCGACGGAGACAGAGAGAGAGCAG	1272
QY	1141	AGCTGCGCGGAGAGGAGAGACAGCAGAACTGAGGAGAGAGTGAATCAACATGG	1200
DB	1273	AGCTGCGCGGAGAGGAGAGACAGCAGAACTGAGGAGAGAGTGAATCAACATGG	1332
QY	1201	ATGAAATTAAGCAGATCTGAGACAGACAAAGCAGAGCCCTGGCAGGGAATGACAGAA	1260
DB	1333	ATGAAATTAAGCAGATCTGAGACAGACAAAGCAGAGCCCTGGCAGGGAATGACAGAA	1392
QY	1261	ACATAGATGTTTTAATGTGAGATCAGAAAGAGACACCATTAATTTACTTATCAGC	1320
DB	1393	ACATAGATGTTTTAATGTGAGATCAGAAAGAGACACCATTAATTTACTTATCAGC	1452
QY	1321	GTGAAAGCGGATCATACCTGTGAATTTGAATTTGAATTTCAATTTCAACACAGGCGC	1380
DB	1453	GTGAAAGCGGATCATACCTGTGAATTTGAATTTGAATTTCAATTTCAACACAGGCGC	1512
QY	1381	GAGAGATGACTTTAAATGTTTATGAGGAGTGAATTTGAAACTGTAATTTACTA	1440
DB	1513	GAGAGATGACTTTAAATGTTTATGAGGAGTGAATTTGAAACTGTAATTTACTA	1572
QY	1441	ATAAATTTGATCATCTGAAGATGATTTTGAATTTTATGATGACATTTGTAGGAA	1500
DB	1573	ATAAATTTGATCATCTGAAGATGATTTTGAATTTTATGATGACATTTGTAGGAA	1632
QY	1501	AAATGGAATGCTTTTAAACAGCTTTTGGGGGTACTTTGGAAGTGTCTAATAAGTG	1560
DB	1633	AAATGGAATGCTTTTAAACAGCTTTTGGGGGTACTTTGGAAGTGTCTAATAAGTG	1692
QY	1561	TCAATTTTGGTAGTAGTATTTGTTGAGAGCTCAACACCAAACTGGAAGATAGTT	1620
DB	1693	TCAATTTTGGTAGTAGTATTTGTTGAGAGCTCAACACCAAACTGGAAGATAGTT	1752
QY	1621	CTCTTCAAGTGTGCGCAGAGCGGCGCTTCTGATTTGGATTAATTAATTTGTGTAAT	1680
DB	1753	CTCTTCAAGTGTGCGCAGAGCGGCGCTTCTGATTTGGATTAATTAATTTGTGTAAT	1812
QY	1681	TACAGCCACCTATAGAGAGTCCATCTGCTGAGAGAGAGACAGAGAACTCTGGGTT	1740
DB			

diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.

Claim #: SEQ ID NO 12356; 2537pp + Sequence Listing; English.

The present invention describes primer sets for synthesizing 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and cDNAs easily without any specialised methods. AAH03166 to AAH95193, AAH13633 to AAH16742 represent human cDNA sequences; AAH92446 to AAH93631 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.

Sequence 3045 BP; 895 A; 642 C; 813 G; 695 T; 0 U; 0 Other;

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every Match      99.3%; Score 2997; DB 4; Length 3045;
1st Local Similarity 99.8%; Pred. No. 0;
Matches 3011; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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[illegible]

QY 1381 GAAGAGATGATCTTTAAATGTTCTATGAGGAGCTGAATAGTGAATCTGTAATATGACTA 1440
 Db 1410 GAAGAGATGATCTTTAAATGTTCTATGAGGAGCTGAATAGTGAATCTGTAATATGACTA 1469
 QY 1441 AATAAATGTACATCTGAGATGATTAATGTGAATTTTGTAGTATGACATTTCTGTAGGA 1500
 Db 1470 AATAAATGTACATCTGAGATGATTAATGTGAATTTTGTAGTATGACATTTCTGTAGGA 1529
 QY 1501 AATAAATGTACATCTGAGATGATTAATGTGAATTTTGTAGTATGACATTTCTGTAGGA 1560
 Db 1530 AATAAATGTACATCTGAGATGATTAATGTGAATTTTGTAGTATGACATTTCTGTAGGA 1589
 QY 1561 TACAAATTTTGTAGTATGATTTTGTAGTATGATTTTGTAGTATGATTTTGTAGTATGATTT 1620
 Db 1590 TACAAATTTTGTAGTATGATTTTGTAGTATGATTTTGTAGTATGATTTTGTAGTATGATTT 1649
 QY 1621 CTCTCTCAAGTGTGGGAGAGCTTTGGGGGCTTTGGGGGCTTTGGGGGCTTTGGGGGCTTT 1680
 Db 1650 CTCTCTCAAGTGTGGGAGAGCTTTGGGGGCTTTGGGGGCTTTGGGGGCTTTGGGGGCTTT 1709
 QY 1681 TAACAGGACCTATAGAGAGTCCATCTGCTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
 Db 1710 TAACAGGACCTATAGAGAGTCCATCTGCTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 1769
 QY 1741 GGTGTCTCTGCTGCTGTACCAAGTGTGGTGGAGGCTGTACCTGTCTCACTG 1800
 Db 1770 GGTGTCTCTGCTGCTGTACCAAGTGTGGTGGAGGCTGTACCTGTCTCACTG 1829
 QY 1801 AAGAGTCTGGCTAATGCTCTGTGTAGTCACTCTGATTTGACATCAATCAATCAATG 1860
 Db 1830 AAGAGTCTGGCTAATGCTCTGTGTAGTCACTCTGATTTGACATCAATCAATCAATG 1889
 QY 1861 GCTAGAGCATGACTGTTTAAACAAAGCTCACTAGCAAGTGAAGAGAGAGAGAGAGAGAGAG 1920
 Db 1890 GCTAGAGCATGACTGTTTAAACAAAGCTCACTAGCAAGTGAAGAGAGAGAGAGAGAGAGAG 1949
 QY 1921 AATACAAAGCTGTTCTGTGTGAGATTTTAAAGGCTGCTGTATATATACCTTTG 1980
 Db 1950 AATACAAAGCTGTTCTGTGTGAGATTTTAAAGGCTGCTGTATATATACCTTTG 2009
 QY 1981 CATTTTAAATGTACAAAGCTATTAAAGTGGCTTGAATTTGAACATTTGTGCTTTAT 2040
 Db 2010 CATTTTAAATGTACAAAGCTATTAAAGTGGCTTGAATTTGAACATTTGTGCTTTAT 2069
 QY 2041 TTACTTTGCTTGTGTGGGCAAGCAACATCTCCCTTAATATATATTACCAAGAA 2100
 Db 2070 TTACTTTGCTTGTGTGGGCAAGCAACATCTCCCTTAATATATATTACCAAGAA 2129
 QY 2101 GCAAGAGCATGATTTAGTATTTTGAACAAACAAAGGCAAGAGGGGCTGACCTGGAGC 2160
 Db 2130 GCAAGAGCATGATTTAGTATTTTGAACAAACAAAGGCAAGAGGGGCTGACCTGGAGC 2189
 QY 2161 AGAGCATGTTGAGAGGCAAGGCTGAGAGGGCAAGTTTGTGTGGACAGATCTGTGCT 2220
 Db 2190 AGAGCATGTTGAGAGGCAAGGCTGAGAGGGCAAG-TTTGTGTGGACAGATCTGTGCT 2248
 QY 2221 ACTTTATCTGGAGTAAAGAAACAAAGTTCATTGATGTGGAAGATATATACAGTGT 2280
 Db 2249 ACTTTATCTGGAGTAAAGAAACAAAGTTCATTGATGTGGAAGATATATACAGTGT 2308
 QY 2281 TAGAATTTAGGAGCTTTAGAAAACAGGAATACATGTTGTTTTATCATAGTGTACA 2340
 Db 2309 TAGAATTTAGGAGCTTTAGAAAACAGGAATACATGTTGTTTTATCATAGTGTACA 2368

QY 2341 CATTTAGCTTGTGTAAATGACTCAAAAAGTCAATTTAAATCAAGTCAATGTGAATTT 2400
 Db 2369 CATTTAGCTTGTGTAAATGACTCAAAAAGTCAATTTAAATCAAGTCAATGTGAATTT 2428
 QY 2401 TGAATAATTAAGTAAATCAATTAATCAATTAATCAATTAATCAATTAATCAATTAATCAAT 2460
 Db 2429 TGAATAATTAAGTAAATCAATTAATCAATTAATCAATTAATCAATTAATCAATTAAT 2488
 QY 2461 GGTTCCTAGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2520
 Db 2489 GGTTCCTAGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2548
 QY 2521 ATTAATGACTGACTTCCAGTAAGGCTCTCTAAGGGTAAAGTGAAGGATCCACAGGATTT 2580
 Db 2549 ATTAATGACTGACTTCCAGTAAGGCTCTCTAAGGGTAAAGTGAAGGATCCACAGGATTT 2608
 QY 2581 TGAGATGCTAAGGCCCCAGAGATCGTTTGAACCAACCCCTCTTATTTTCAGAGGGGAAAT 2640
 Db 2609 TGAGATGCTAAGGCCCCAGAGATCGTTTGAATCCACCCCTCTTATTTTCAGAGGGGAAAT 2668
 QY 2641 GGGGGCTAGAGATTAAGAGATCAAGGATCAAGGATCAAGGATCAAGGATCAAGGATCAAG 2700
 Db 2669 GGGGGCTAGAGATTAAGAGATCAAGGATCAAGGATCAAGGATCAAGGATCAAGGATCAAG 2728
 QY 2701 TCCCGAGTGTGGGAGCTACAGGATCAAGGATCAAGGATCAAGGATCAAGGATCAAGGATCA 2760
 Db 2729 TCCCGAGTGTGGGAGCTACAGGATCAAGGATCAAGGATCAAGGATCAAGGATCAAGGATCA 2788
 QY 2761 GCTGCAAGCTCCAACTTAAACATTTCTCATATGTGATGCTTGTAGTCAATAGGTTAAAC 2820
 Db 2789 GTTGCAAGCTCCAACTTAAACATTTCTCATATGTGATGCTTGTAGTCAATAGGTTAAAC 2848
 QY 2821 TTTCCAGCCCAAGAAAGGCAACTTAGTAATAATTTTAGAGTACTTTTCACTCTCTTAAG 2880
 Db 2849 TTTCCAGCCCAAGAAAGGCAACTTAGTAATAATTTTAGAGTACTTTTCACTCTCTTAAG 2908
 QY 2881 TCTCTTCCAGCTCACTTTTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2940
 Db 2909 TCTCTTCCAGCTCACTTTTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2968
 QY 2941 TCATAAAGTCTCTATTTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3000
 Db 2969 TCATAAAGTCTCTATTTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3028
 QY 3001 AATGTTCTGTCACTT 3017
 Db 3029 AATGTTCTGTCACTT 3045

RESULT 6

ACC50169 standard; cDNA; 3042 BP.

XX ACC50169;
 XX ACC50169;

12-JUN-2003 (first entry)

XX
 DE Breast cancer associated cDNA sequence SEQ ID NO:183.
 KW Human; breast cancer; cytostatic; gene therapy; gene; ss.
 XX Homo sapiens.
 OS

Db	1148	AAAGCTGCGCGGGGAAGGGAGAAACACGACAGAACTGAGAGGAGAGAAATGACTTACACATGG	-207
Qy	1201	ATGAAAAATGAGCGAGAACTGAGCGAGACAGCAGACGAGCCCTGGCAGGGAAATGACAGA	-260
Db	1208	ATGAAAAATGAGCGAGAACTGAGCGAGACAGCAGAGAGCGCCCTGGCAGGGAAATGACAGA	-1267
Qy	1261	ACATAGATGTTTTTAATGTTGAAGTCAGAAAAGAGACACCTAAATTTACTTGCATCAGC	-1320
Db	1268	ACATAGATGTTTTTAATGTTGAAGTCAGAAAAGAGACACCATTAATTTACTTGATCAGC	-1327
Qy	1321	GTGAAAAGCGGAATCATACACTCTGAATTGAACATGGAAATCACATATTTTCACACAGGGCC	-1380
Db	1328	GTGAAAAGCGGAATCATACACTCTGAATTGAACATGGAAATCACATATTTTCACACAGGGCC	-1387
Qy	1351	GAAAGATGACTTTAAATGTTGATGGGAGCTGAATCTGAAAATCTGTGAATGTACTA	-1440
Db	1386	GAAAGATGACTTTAAATGTTGATGGGAGCTGAATCTGAAAATCTGTGAATGTACTA	-1447
Qy	1441	AATAAATGTACATCTGAAGATGATTAATGTGAATTTTAGTATGCACTTTGTGTAGAA	-1500
Db	1448	AATAAATGTACATCTGAAGATGATTAATGTGAATTTTAGTATGCACTTTGTGTAGAA	-1507
Qy	1501	AAATGGAATGGTCTTTTAAACAGCTTTT-GGGGGGTACTTT-GGAAGTGTCTAATAGGT	-1559
Db	1508	AAATGGAATGGTCTTTTAAACAGCTTTTGGGGGGTACTTTGGAAGTGTCTAATAGGT	-1567
Qy	1560	GTACAAATTTTTGGTAGTAGGTATTCGTGAGAGAGTCTCAACACCMAACTGCAACATAGT	-1619
Db	1566	GTCAAAATTTTTGGTAGTAGGTATTCGTGAGAGAGTCTCAACACCMAACTGCAACATAGT	-1627
Qy	1620	TCTCTTTCAAGTGTGGCGACAGCGGGGCTTCCTGATTCGSAATATACATTTGTGTAA	-1679
Db	1628	TCTCTTTCAAGTGTGGCGACAGCGGGGCTTCCTGATTCGSAATATACATTTGTGTAA	-1687
Qy	1680	TTAAGCAGCAOCTATAGAGAGTCCATCTGCTGTGAAGGAGACAGAGACTCTGGGTT	-1739
Db	1688	TTAAGCAGCAOCTATAGAGAGTCCATCTGCTGTGAAGGAGACAGAGACTCTGGGTT	-1747
Qy	1740	CGTGCTGCTGTCCAGTGTCTACAGTGGTGGTCCAGCCTGTACTGTCTCTACT	-1799
Db	1748	CGTGCTGCTGTCCAGTGTCTACAGTGGTGGTCCAGCCTGTACTGTCTCTACT	-1807
Qy	1800	GAAAAGTGGCTTAATGCTCTGTGTAGTCACTCTGATTCAGCAATCAATCAAT	-1859
Db	1808	GAAAAGTGGCTTAATGCTCTGTGTAGTCACTCTGATTCAGCAATCAATCAAT	-1867
Qy	1860	GGCCTAGAGCACTGATGTGTAAACAAGAGTCACTACAAAGTAGCAACAGCTTTAAGTC	-1919
Db	1868	GGCCTAGAGCACTGATGTGTAAACAAGAGTCACTACAAAGTAGCAACAGCTTTAAGTC	-1927
Qy	1920	TAAATACAAAGTGTCTGTGTGAGAAATTTTTTAAAGGCTACTGTATATATACCCCTG	-1979
Db	1928	TAAATACAAAGTGTCTGTGTGAGAAATTTTTTAAAGGCTACTGTATATATACCCCTG	-1987
Qy	1980	TCATTTTAATGTACAAACGGCTATTAAAGTGGCTTGAATTTGAACATTTGTGCTTTTA	-2039
Db	1988	TCATTTTAATGTACAAACGGCTATTAAAGTGGCTTGAATTTGAACATTTGTGCTTTTA	-2047
Qy	2040	TTTACTTTGCTTCTGTGTGGGCAAGCAACATCTTCCTAAATATATATACCAAGAA	-2099
Db	2048	TTTACTTTGCTTCTGTGTGGGCAAGCAACATCTTCCTAAATATATATACCAAGAA	-2107

Qy	2100	AGCAAGAGCTAGATTAGCTTTTTCAGCAAAACAAGGCCAAAGGGGGCTGACCTGGAG	2150
Ds	2108	AGCAAGAGCGAGATTAGCTTTTTCAGCAAAACAAGGCCAAAGGGGGCTGACCTGGAG	2167
Qy	2160	CAGAGCATGGTCAGAGGCAAGGCAAGGAGGCAAGGCTTTCTGTGCGACAGATCTGTGC	2219
Ds	2168	CAGAGCATGGTCAGAGGCAAGGCAAGGAGGCAAGGCTTTCTGTGCGAGATCTGTGCC	2226
Qy	2220	TACTTTATTACTGGAGTAAAGAAAACAAGTTCATTCATGTCGGAAGGATATACAGTG	2279
Ds	2227	TACTTTATTACTGGAGTAAAGAAAACAAGTTCATTCATGTCGGAAGGATATACAGTG	2286
Qy	2280	TTAGAAATTAAGGACTGTTTAGAAAACAGGAATCAATAGGTGTTTTTATCCTAGTGTAC	2339
Ds	2287	TTAGAAATTAAGGACTGTTTAGAAAACAGGAATCAATAGGTGTTTTTATCCTAGTGTAC	2346
Qy	2340	ACATTTAGCTGTGCTGAATAGCTCACAAAACCTGATTTTAAATCAAGTAAATCTGATTT	2399
Ds	2347	ACATTTAGCTGTGCTGAATAGCTCACAAAACCTGATTTTAAATCAAGTAAATCTGATTT	2406
Qy	2400	TTGAAAATTAAGTACTTAATCTTAATTCACAAATCAATGGGATTAAGTTTTCAGTTGAGT	2459
Ds	2407	TTGAAAATTAAGTACTTAATCTTAATTCACAAATCAATGGGATTAAGTTTTCAGTTGAGT	2466
Qy	2460	TGGTTCTTAGTATTATTTATGGTAATAGGCTCTTACACCTTGCATAAATCACTGCCACAT	2519
Ds	2467	TGGTTCTTAGTATTATTTATGGTAATAGGCTCTTACACCTTGCATAAATCACTGCCACAT	2526
Qy	2520	CATTATAGCTGACTCCAGTAGAGGCTCTTAAGGGGTAAAGTAGGAGTCCACAGAT	2579
Ds	2527	CATTATAGCTGACTCCAGTAGAGGCTCTTAAGGGGTAAAGTAGGAGTCCACAGAT	2586
Qy	2580	TTGAGATGCTTAAGGCCOCCAGAGATCGTTTTGAACCAACCCCTCTTATTTTCAGAGGGGAAA	2639
Ds	2587	TTGAGATGCTTAAGGCCOCCAGAGATCGTTTTGAACCAACCCCTCTTATTTTCAGAGGGGAAA	2646
Qy	2640	TGGGGCTTAAGATTTACAGAGCATCTAGCTGGTGGCTGGACACCCCTGGCTCACACAGA	2699
Ds	2647	TGGGGCTTAAGATTTACAGAGCATCTAGCTGGTGGCTGGACACCCCTGGCTCACACAGA	2706
Qy	2700	CTCCGAGTAGCTGGGACTACAGGCAACAGTCACTGAAGCAGGCGCTGTTGCAATTCA	2759
Ds	2707	CTCCGAGTAGCTGGGACTACAGGCAACAGTCACTGAAGCAGGCGCTGTTGCAATTCA	2766
Qy	2760	CGCTGCCACCTCCAACTTAAGCAATCTTCATATGTGATGCTCTTCTAGTCACTAAGGTAAA	2819
Ds	2767	CGTGGCCACCTCCAACTTAAGCAATCTTCATATGTGATGCTCTTCTAGTCACTAAGGTAAA	2826
Qy	2820	CTTTCOCCACGAAAGAGGCACTTAGATAAATCTTAGAGTACTTTCTGACTCTCTCAA	2879
Ds	2827	CTTTCOCCACGAAAGAGGCACTTAGATAAATCTTAGAGTACTTTCTGACTCTCTCAA	2886
Qy	2880	GTCCCTTCCAGCTCCACTTTGAGTCTCTCTTGGGGTTGATAGGAATTTTCTCTTGCTTT	2939
Ds	2887	GTCCCTTCCAGCTCCACTTTGAGTCTCTCTTGGGGTTGATAGGAATTTTCTCTTGCTTT	2946
Qy	2940	CTCAATAAGTCTCTATTCATCTCATCTTTAAATTTGTACGCAATAGAAATGCTGAGAAA	2999
Ds	2947	CTCAATAAGTCTCTATTCATCTCATCTTTAAATTTGTACGCAATAGAAATGCTGAGAAA	3006
Qy	3000	AAATGTTCTGTTCAACTTT	3017
Ds	3007	AAATGTTCTGTTCAACTTT	3024

RESULT 7

ADB75331
ID ADB75331 standard; cDNA; 3042 BP.

XX

AC ADB75331;

XX

DT 04-DEC-2003 (first entry)

XX

DE Prostate cancer marker cDNA.

XX

KW Prostate; cancer; cytostatic; gene therapy; marker; ss.

XX

OS Homo sapiens.

XX

PN W0200309814-A2.

XX

PD 06-FEB-2003.

XX

XX 25-JUL-2002; 2002W0-US023913.

XX

PR 25-JUL-2001; 2001US-0307982P.

PR

PR 22-AUG-2001; 2001US-0314356P.

PR

PR 25-SEP-2001; 2001US-032520P.

PR

PR 12-DEC-2001; 2001US-0341746P.

PR

PR 05-MAR-2002; 2002US-0362158P.

XX

PA (MILL-) MILLENNIUM PHARM INC.

XX

PI Schlegel R, Monahan JE, Endege WO, Gannavarapu M, Gorbacheva B;

PI Hoersht S, Kamatkar S, Womsey AM, Glatt K, Zhao X, Anderson D;

XX

XX WPI; 2003-248033/24.

DR

XX New nucleic acid molecule, useful for diagnosing or treating prostate

PT

PT cancer.

XX

PS Disclosure; SEQ ID NO 155; 99pp; English.

XX

XX The invention relates to newly discovered cancer markers associated with
the cancerous state of prostate cells. Also disclosed is a method of
assessing whether a patient is afflicted with prostate cancer. The method
of the invention involves assessing whether a patient is afflicted with
prostate cancer by comparing the level of expression of a marker in a
patient sample and the normal level of expression of the marker in a
control non-prostate cancer sample, where a significant increase in the
level of expression of the marker in the patient sample and the normal
level indicates that the patient is afflicted with prostate cancer.

XX Nucleic acids of the invention are useful for diagnosing or treating
prostate cancer, and may be useful in gene therapy. Sequences given in
ADB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences.

XX

XX Sequence 3042 BP; 910 A; 635 C; 502 G; 695 T; C U; 0 Other;

SQ

Query Match

Best Local Similarity 99.0%; Score 2987.6; DB 9; Length 3042;

Matches 3012; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

QY

1 GCTGGGCGCAAGCGCGGAGCGCGGCGGAGCTCGAGGCGGCGGCGGCGGAGCGGACC 60

Db 8 GCTGGGCGCAAGCGCGGAGCGCGGCGGAGCGCGGCGGCGGAGCGGAGCGACC 67
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 RESULT 8
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 XX
 DT 15-JAN-2004 (first entry)
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 DE Human prostate cancer: diagnosis related DNA sequence SegID114.
 XX
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 KW male cancer-related death; serum biomarker; tissue biomarker; cytostatic;
 KW gene therapy; prostate biopsy tissue; AMACR;
 KW alpha-methylacyl-coenzyme A racemase; diagnosing cancer; cell growth;
 KW human; ds.
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 PD 13-FEB-2003.
 XX
 PF 02-AUG-2002; 2002W0-US024567.
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 PR 15-NOV-2001; 2001US-0334468P.
 PR 01-AUG-2002; 2002US-00210120.
 XX
 PA (UNMI) UNIV MICHIGAN.
 XX
 PI Rubin MA, Chinnaiyan AM, Sreekumar A;
 XX
 DR WPI; 2003-278396/27.
 XX
 PT Characterizing prostate tissue comprises providing a prostate tissue
 sample from a subject and detecting the presence or absence of expression
 of hepsin, p1m-1 or E2H2.
 XX
 PS Disclosure; SEQ ID NO 114; 297pp; English.
 XX
 CC This invention relates to a novel method of characterising prostate
 tissue in a subject and to compositions and methods for cancer
 diagnostics, including cancer markers, in particular prostate cancer.
 CC Prostate cancer (PCA) is a leading cause of male cancer-related death.
 CC Additional serum and tissue biomarkers would aid diagnosis. The invention
 may provide means of producing compounds with a cytostatic activity or
 allow the development of gene therapy. The methods of the invention
 are useful for characterising prostate tissue in a subject, screening

CC compounds, characterising inconclusive prostate biopsy tissue in a
 subject, detecting AMACR (alpha-methylacyl-coenzyme A racemase),
 CC expression in a bodily fluid, characterising tissue in a subject,
 CC diagnosing cancer in a subject and inhibiting the growth of cells. The
 CC present sequence is a DNA sequence which is preferably utilised in the
 CC method of the invention.
 XX
 SQ Sequence 3042 BP; 910 A; 635 C; 802 G; 695 T; 0 U; 0 Other;
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 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 3012; Conservative 0; Mismatches 4; Indels 2; Gaps 2;
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	2987.6	99.0	3042	14	US-10-205-823-155
3	2987.6	99.0	3042	14	US-10-177-293-183
4	2987.6	99.0	3042	14	US-10-210-120-114
5	2987.6	99.0	3042	15	US-10-341-434-120
					Sequence 1654, Ap
					Sequence 155, App
					Sequence 183, App
					Sequence 114, App
					Sequence 120, App

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; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-1654

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Best Local Similarity 99.8%; Pred. No. 0;
Matches 3012; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

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Db 728 ACGACCAAGACAGCAGCTCCAGGCCCTCACTGAGCTCAGCCAGGCTGCAGGCGACAG 787
QY 781 GCGTGCACACACAGAGGTGCCAAGAGGAGGAAAGCTGTGTTAAACAGCAAGATGCC 840
Db 788 GCGTGCACACACAGAGGTGCCAAGAGGAGGAAAGCTGTGTTAAACAGCAAGATGCC 847
QY 841 AGACACAGCCOCTCACTCCGAACTGTGTTTGGATCAAGAGACAGATTTGAGAAAGG 900
Db 848 AGACACAGCCOCTCACTCCGAACTGTGTTTGGATCAAGAGACAGATTTGAGAAAGG 907
QY 901 AAAACCAATGAGATCCAGTTSSTGAATGAGAGGCTCAGAGGACAGGCTGCCGCGAGAGC 960
Db 908 AAAACCAATGAGATCCAGTTSSTGAATGAGAGGCTCAGAGGACAGGCTGCCGCGAGAGC 967
QY 961 CAGGCGGAGACAGCTGTGTAAGACAGAGCTGTAGTGGAGAGGCTTGGGSGGAGCG 1020
Db 968 CAGGCGGAGACAGCTGTGTAAGACAGAGCTGTAGTGGAGAGGCTTGGGSGGAGCG 1027
QY 1021 GAGAACTGGGCCACAGCCACAGAGTSCAGGCTGCCCTGTCACTGAGCCAGGAAAATCCAG 1080
Db 1028 GAGAACTGGGCCACAGCCACAGAGTSCAGGCTGCCCTGTCACTGAGCCAGGAAAATCCAG 1087
QY 1081 AGATGAGGGGCCCTGAGCGAGACAGAGCTTGTATCCCGGACGGAACAGAGGAGAGCAGG 1140
Db 1088 AGATGAGGGGCCCTGAGCGAGACAGAGCTTGTATCCCGGACGGAACAGAGGAGAGCAGG 1147
QY 1141 AAGCTGCGGGGAGGAGAACCCAGCAGAACTGAGGAGAGAGTGAAGTACACATGG 1200
Db 1148 AAGCTGCGGGGAGGAGAACCCAGCAGAACTGAGGAGAGAGTGAAGTACACATGG 1207
QY 1201 ATGAAATGAAGAGAGATCTGAGACAGACAAAGAGCGGCTGGCAGGGAATGACAGAA 1260
Db 1208 ATGAAATGAAGAGAGATCTGAGACAGACAAAGAGCGGCTGGCAGGGAATGACAGAA 1267
QY 1261 ACATAGATTTTTTAATGTTGAAGATCAGAAAGAGACACATTAATTTACTTGCATCAGC 1320
Db 1268 ACATAGATTTTTTAATGTTGAAGATCAGAAAGAGACACATTAATTTACTTGCATCAGC 1327
QY 1321 GTGAAAAGGGGAATCATACACTCTGAATTCGAACTGGATCAATATTTCAACACAGGCC 1380
Db 1328 GTGAAAAGGGGAATCATACACTCTGAATTCGAACTGGATCAATATTTCAACACAGGCC 1387
QY 1381 GAGAGATGACTTTTAAATGTTTATGAGGAGCTGAATACAGAAAGTGTGAATGTACTA 1440
Db 1388 GAGAGATGACTTTTAAATGTTTATGAGGAGCTGAATACAGAAAGTGTGAATGTACTA 1447
QY 1441 AATAAATGTACATCTGAGATGATTATGTGAATTTTAAATGATGACCTTTGTAGGAA 1500
Db 1448 AATAAATGTACATCTGAGATGATTATGTGAATTTTAAATGATGACCTTTGTAGGAA 1507
QY 1501 AAAATGGAATGCTTTTAAACAGCTTTTGGGGGTACTTTGGAAGTGTCTAATTAAGT 1559
Db 1508 AAAATGGAATGCTTTTAAACAGCTTTTGGGGGTACTTTGGAAGTGTCTAATTAAGT 1567
QY 1560 GTCACAATTTTGTAGTATGTTTGTGAGAGGCTCAACACAAACCTGGAACATAGT 1619
Db 1568 GTCACAATTTTGTAGTATGTTTGTGAGAGTTCACACCAAACTGGAACATAGT 1627
QY 1620 TCTCCTTCAAGTGTGGCGACAGCGGGGCTTCCTGATCTGGAATATACTTTGTAAA 1679

Db 2587 TTGAGATCTAAGGCCCCAGAGATCGTTTGATCCAAACCCCTCTTATTTTTCAGAGGGGAAA 2646
Qy TGGGGCTTAGAGTTACAGAGCATCTAGCTGGTGGCACCCCTGGCTTCACACAGA 2699
Db TGGGGCTTAGAGTTACAGAGCATCTAGCTGGTGGCACCCCTGGCTTCACACAGA 2706
Qy CTCGGAGTAGTGGGACTACAGGACACAGTCACTGAGGAGGCGCTCTTTGCAATCA 2759
Db CTCGGAGTAGTGGGACTACAGGACACAGTCACTGAGGAGGCGCTCTTTGCAATCA 2766
Qy CGGTGCGACCTCCAACTTAACATCTTCATATGATGATCTCTTAGTCACTAAGTTAA 2819
Db CGGTGCGACCTCCAACTTAACATCTTCATATGATGATCTCTTAGTCACTAAGTTAA 2826
Qy CTTTCCACACAGAAAGGCACTTAGATATAAATCTTAGAGTACTTTCATCTCTTAA 2879
Db CTTTCCACACAGAAAGGCACTTAGATATAAATCTTAGAGTACTTTCATCTCTTAA 2886
Qy GTCTCTTCCAGGCTCACTTTAGTCTCTCTGGGTTGATAGAAATTTCTCTGCTT 2939
Db GTCTCTTCCAGGCTCACTTTAGTCTCTCTGGGTTGATAGAAATTTCTCTGCTT 2946
Qy CTGATTAAGTCTTAATCACTCACTGATATAAATCTTAGAGTACTTTCATCTCTTAA 2999
Db CTGATTAAGTCTTAATCACTCACTGATATAAATCTTAGAGTACTTTCATCTCTTAA 3006
Qy 3000 AAATGTTCTGTTCACTT 3017
Db 3007 AAATGTTCTGTTCACTT 3024

RESULT 2
US-10-205-823-155
; Sequence 155, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Heersche, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Monsey, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158

; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 155
; LENGTH: 3042
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-205-823-155

Query Match 99.0%; Score 2987.6; DB 14; Length 3042;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3012; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

Qy 1 GCTGGGGGCGACGCGCGGAGGCGCGGAGCTCGAGGCGGCGGCGGCGGCGGAGAGGAGC 60
Db 8 GCTGGGGGCGACGCGCGGAGGCGCGGAGCTCGAGGCGGCGGCGGCGGCGGAGAGGAGC 67
Qy 61 CGGGGGGCGCTGTAGCGGGGCGCGGATCCCGAGTGGCGGCGCGGAGCTCGAGGAGGAGC 120
Db 68 CGGGGGGCGCTGTAGCGGGGCGCGGATCCCGAGTGGCGGCGCGGAGCTCGAGGAGGAGC 127
Qy 121 TTCTCAGGCGCTGATTTTGAATGATGGGCTTGGGAAAGCGGGGCTCGACGATGAGTCCG 180
Db 128 TTCTCAGGCGCTGATTTTGAATGATGGGCTTGGGAAAGCGGGGCTCGACGATGAGTCCG 187
Qy 181 CGGGCGCTGTGGCGGCGCTGTGGGCTGATCATCTCTTGGGCTTCACTACTGGA 240
Db 188 CGGGCGCTGTGGCGGCGCTGTGGGCTGATCATCTCTTGGGCTTCACTACTGGA 247
Qy 241 TTGGGAGCTCCCGGAGCGTGGAGCTTCCAGACACGAGATCAATGGAGCTCGAGGAGGCTC 300
Db 248 TTGGGAGCTCCCGGAGCGTGGAGCTTCCAGACACGAGATCAATGGAGCTCGAGGAGGCTC 307
Qy 301 GCAGGGGCGCTGCGAGAGAGGCGCGTGGAGCTGAGAGAGAAAGAGTTCAGGAGGAGC 360
Db 308 GCAGGGGCGCTGCGAGAGAGGCGCGTGGAGCTGAGAGAGAAAGAGTTCAGGAGGAGC 367
Qy 361 TGGAGAGGAGCGGAGGAGGCTTGACAAATCCAGTCCAGGCGACAACTTCCAGCTGAGGA 420
Db 368 TGGAGAGGAGCGGAGGAGGCTTGACAAATCCAGTCCAGGCGACAACTTCCAGCTGAGGA 427
Qy 421 GCGTCAAGAGCTGTACAGAGAGGAGGCGGTTTGGTGAATTAACATCAACAGAGTG 480
Db 428 GCGTCAAGAGCTGTACAGAGAGGAGGCGGTTTGGTGAATTAACATCAACAGAGTG 487
Qy 481 AGAGGCTCATCCGAGTGTGCAAGACCGATTAAAGACCTCGAGAGGAGTACGGGAGC 540
Db 488 AGAGGCTCATCCGAGTGTGCAAGACCGATTAAAGACCTCGAGAGGAGTACGGGAGC 547
Qy 541 TGCAGCAGGATGCTCCAGTTTTCAGAGAACAGACCACTCGAGAGGAGTCTCCT 600
Db 548 TGCAGCAGGATGCTCCAGTTTTCAGAGAACAGACCACTCGAGAGGAGTCTCCT 607
Qy 601 ACGAGCTGAGGCGCTGATCAATCAGATGAGGAGGTGAGGAGACGCTGAGGAGGAGG 660
Db 608 ACGAGCTGAGGCGCTGATCAATCAGATGAGGAGGTGAGGAGACGCTGAGGAGGAGG 667
Qy 661 TAGAGAGGCTCAACAAAGGAGATGAGGAGTGTAGCTTCAGAGAGCTGAGTGAARACA 720
Db 668 TAGAGAGGCTCAACAAAGGAGATGAGGAGTGTAGCTTCAGAGAGCTGAGTGAARACA 727
Qy 721 ACGAGCAGGAGGAGGCTCCAGGCTCAGTGGGCTTCCAGGCGGAGGCTGAGGAGGAG 780

Db 728 ACAGACAGACAGAGAGCTCCAAAGCCCTCAGTGAAGCCTCAGGCCACGGCTGAGAGCAGAG 787
Qy 761 GCGTCCACACACAGAGGTGCCAAAGAGGAGGAAACGCTGCTTGTAAACAGCAAGTCCC 840
Db 788 GCGTCCACACACAGAGGTGCCAAAGAGGAGGAAACGCTGCTTGTAAACAGCAAGTCCC 847
Qy 841 AGACACACAGCCCGAAGTCCGAAAGTGGTTTGGATTCAAAGAGACAAAGTTGAGAAAGAG 900
Db 846 AGACACACAGCCCGAAGTCCGAAAGTGGTTTGGATTCAAAGAGACAAAGTTGAGAAAGAG 907
Qy 901 AAACCAATGATGATCCAGAGTGGTGAATGAGAGAGCTCAGAGGACAGAGGCTGCCGACAGAGC 960
Db 908 AAACCAATGATGATCCAGAGTGGTGAATGAGAGAGCTCAGAGGACAGAGGCTGCCGACAGAGC 967
Qy 961 CAGGCGGGGACAGAGTGGTGAAGACAGAGCTGTAGTGGAGAGGCTTCGGGGGAGAGCG 1020
Db 968 CAGGCGGGGACAGAGTGGTGAAGACAGAGCTGTAGTGGAGAGGCTTCGGGGGAGAGCG 1027
Qy 1021 GAGACTGGGCGAGACCCACAGAGTGGAGGCTGGAGGCTGGCTGTCACTGAGCCAGGAAATCCAG 1080
Db 1028 GAGAACTGGGCGAGACCCACAGAGTGGAGGCTGGAGGCTGGCTGTCACTGAGCCAGGAAATCCAG 1087
Qy 1081 AGATGAGGGGCTGTAGGCGAGACCCAGAGTGGTCACTCCCGACGACAGAGGAGAGCAGAG 1140
Db 1088 AGATGAGGGGCTGTAGGCGAGACCCAGAGTGGTCACTCCCGACGACAGAGGAGAGCAGAG 1147
Qy 1141 AAGCTGCCGGGAGAGGAGAGAAACAGAGAACTGAGAGAGAGATGATCAACATGG 1200
Db 1148 AAGCTGCCGGGAGAGGAGAGAAACAGAGAACTGAGAGAGAGATGATCAACATGG 1207
Qy 1201 ATGAAATGAGAGAGATCTGAGACAGACAGCAGCAGCCCTGCCAGGGAATGACAGAA 1260
Db 1208 ATGAAATGAGAGAGATCTGAGACAGACAGCAGCAGCCCTGCCAGGGAATGACAGAA 1267
Qy 1261 ACATAGATGTTTTATGTTAGATCAGAAAAGAGACACATTAATTTACTTGATCAGC 1320
Db 1268 ACATAGATGTTTTATGTTAGATCAGAAAAGAGACACATTAATTTACTTGATCAGC 1327
Qy 1321 GTGAAAGGGGAATCATACACTCTGAATGAACTGGAAATCAATATTCACACAGGGCC 1380
Db 1328 GTGAAAGGGGAATCATACACTCTGAATGAACTGGAAATCAATATTCACACAGGGCC 1387
Qy 1381 GAAGAGATGATTTAAATGTTCAAGAGGAGTGAATCTGAAACTGTGAATGTACTA 1440
Db 1388 GAAGAGATGATTTAAATGTTCAAGAGGAGTGAATCTGAAACTGTGAATGTACTA 1447
Qy 1441 AATAAATGTACATCTGAAGATGATTTATGTAATTTTAGTATGCACTTTGTGAGGAA 1500
Db 1448 AATAAATGTACATCTGAAGATGATTTATGTAATTTTAGTATGCACTTTGTGAGGAA 1507
Qy 1501 AAAATGGAATGCTTTTAAACAGCTTTTGGGGGCTACTTTGGAAAGTGTCTAATAGGT 1559
Db 1508 AAAATGGAATGCTTTTAAACAGCTTTTGGGGGCTACTTTGGAAAGTGTCTAATAGGT 1567
Qy 1560 GTCAATTTTTGTAGTGTATTTGCTGAGAGCTCAACACCAAACTGGAAACATAGT 1619
Db 1568 GTCAATTTTTGTAGTGTATTTGCTGAGAGTTCACACCAAACTGGAAACATAGT 1627
Qy 1620 TCTCCCTCAAGTGTGGGACAGCGGGGCTTCTGATTTCTGGAATATACTTTGTGTAAA 1679
Db 1628 TCTCCCTCAAGTGTGGGACAGCGGGGCTTCTGATTTCTGGAATATACTTTGTGTAAA 1687
Qy 1680 TTAAACGCCACCTATAGAGAGTCCATCTGCTGTGAAGAGAGACAGAGAACTCTGGGTT 1739

Db 1688 TTAAACGCCACCTATAGAGAGTCCATCTGCTGTGAAGAGAGACAGAACTCTGGGTT 1747
Qy 1740 CCGTCTCTCTGTCCACGCTGTACCAAGTGTGTCGAGCCCTGTACTGTCTCTACT 1799
Db 1748 CCGTCTCTCTGTCCACGCTGTGTACCAAGTGTGTCGAGCCCTGTACTGTCTCTACT 1807
Qy 1800 GAAAGCTGGCTAATGCTCTGTGTAGTCACTCTGTGATCTGACAAATCAATCAAT 1859
Db 1808 GAAAGCTGGCTAATGCTCTGTGTAGTCACTCTGTGATCTGACAAATCAATCAAT 1867
Qy 1860 GGCCTAGAGCACTGACTGTTAAACACAAAGCTCACTAGCAAAAGTAGCAAGCTTTAAGTC 1919
Db 1868 GGCCTAGAGCACTGACTGTTAAACACAAAGCTCACTAGCAAAAGTAGCAAGCTTTAAGTC 1927
Qy 1920 TAAATACAAAGCTGTTCTGTGTGAGAAATTTTAAAGGCTACTGTGATAATAACCCCTG 1979
Db 1928 TAAATACAAAGCTGTTCTGTGTGAGAAATTTTAAAGGCTACTGTGATAATAACCCCTG 1987
Qy 1980 TCATTTTATGTACAAAGCTATTAAGTGGCTTAGAATTTGAACATTTGTGTCTTTA 2039
Db 1988 TCATTTTATGTACAAAGCTATTAAGTGGCTTAGAATTTGAACATTTGTGTCTTTA 2047
Qy 2040 TTTACTTTGCTTCTGTGTGGGCAAGACACATCTTCCCTAAATATATATATACCAAGAA 2099
Db 2048 TTTACTTTGCTTCTGTGTGGGCAAGACACATCTTCCCTAAATATATATATACCAAGAA 2107
Qy 2100 AGCAAGAGACAGATTAGGTTTTGAACAAACAAACAGGCAAGGCGCTGACCTGGAG 2159
Db 2108 AGCAAGAGACAGATTAGGTTTTGAACAAACAAACAGGCAAGGCGCTGACCTGGAG 2167
Qy 2160 CAGACATGTTGAGGCAAGGCTGAGAGGCGCAAGTTTGTGTGACAGATCTGTGCC 2219
Db 2168 CAGACATGTTGAGGCAAGGCTGAGAGGCGCAAGTTTGTGTGACAGATCTGTGCC 2226
Qy 2220 TACTTTACTCTGGAGTAAAGAAACAAAGTTCATGATCTGAGAGGATATACAGTG 2279
Db 2227 TACTTTACTCTGGAGTAAAGAAACAAAGTTCATGATCTGAGAGGATATACAGTG 2286
Qy 2280 TTAGAAATTAGGACTGTTTGAACAAACAGGATACATGTTGTTTATCATAGTGTAC 2339
Db 2287 TTAGAAATTAGGACTGTTTGAACAAACAGGATACATGTTGTTTATCATAGTGTAC 2346
Qy 2340 ACATTTAGCTGTGTAAATGATCTCAAAACCTGATTTTAAATCAAGTTAATGTGAAT 2399
Db 2347 ACATTTAGCTGTGTAAATGATCTCAAAACCTGATTTTAAATCAAGTTAATGTGAAT 2406
Qy 2400 TTGAAATTTACTACTTAATCTTAATTCACATAACAAAGGCAATTAAGGTTTGAAGT 2459
Db 2407 TTGAAATTTACTACTTAATCTTAATTCACATAACAAAGGCAATTAAGGTTTGAAGT 2466
Qy 2460 TGGTCTTAGTATATTTATGGTAATAGGCTCTTACCACTTGCAATTAATGSCACAT 2519
Db 2467 TGGTCTTAGTATATTTATGGTAATAGGCTCTTACCACTTGCAATTAATGSCACAT 2526
Qy 2520 CATTAATGACTGACTTCCAGTAAGGCTCTCTAAAGGGTAAAGTAGGAGATCCACAGAT 2579
Db 2527 CATTAATGACTGACTTCCAGTAAGGCTCTCTAAAGGGTAAAGTAGGAGATCCACAGAT 2586
Qy 2586 TTGAGATGCTAAGGCCCGCCAGAGATCGTTTGAACCAACCCCTCTATTTCAGAGGGGAAA 2639
Db 2587 TTGAGATGCTAAGGCCCGCCAGAGATCGTTTGAACCAACCCCTCTATTTCAGAGGGGAAA 2646

D6	668	TAGAAGAGGTCA	CCAAAAAGGGAA	TGAAAGCTGTAGCTTCCAGAGACCTGATGTAAAAACA	727
QY	721	ACGACCCAGAGACAGAGCT	CCAGAGCCCTCAGTCAAGGCTCAGGCTCAGGCGCCAGGCTCGAGGCGACGAG	780	
D6	728	ACGACCCAGAGACAGAGCT	CCAGAGCCCTCAGTCAAGGCTCAGGCTCAGGCGCCAGGCTCGAGGCGACGAG	787	
QY	781	GCTTGCCTCACACACAGAGGT	GCACCAAGGAGGAGAAAGCTGCTTGGTAAACACAAATGCC	840	
D6	788	GCTTGCCTCACACACAGAGGT	GCACCAAGGAGGAGAAAGCTGCTTGGTAAACACAAATGCC	847	
QY	841	AGACACCAAGCCGCCAGTTC	CCAGATGAGTGTGTTTGGATTCAAGAGACAGATTGAGAAAGAGG	900	
D6	848	AGACACCAAGCCGCCAGTTC	CCAGATGAGTGTGTTTGGATTCAAGAGACAGATTGAGAAAGAGG	907	
QY	901	AAACCCATGAGATCCAGTGT	GATGATGAGAGGCTTCCAGGACAGGCTCCGCGCAGAGG	960	
D6	908	AAACCCATGAGATCCAGTGT	GATGATGAGAGGCTTCCAGGACAGGCTCCGCGCAGAGG	967	
QY	961	CAGGCGCGGACAGAGTGT	GGAAAGACAGTCTGTAGGTGGAAGAGGCTTCGSGGAGAGCG	1020	
D6	968	CAGGCGCGGACAGAGTGT	GGAAAGACAGTCTGTAGGTGGAAGAGGCTTCGSGGAGAGCG	1027	
QY	1021	GAGAACTGGGCCAGACCC	CCACAGGTCCAGGCTGCCTCTCAGGTGAGCCAGAAAAATCCAG	1080	
D6	1028	GAGAACTGGGCCAGACCC	CCACAGGTCCAGGCTGCCTCTCAGGTGAGCCAGAAAAATCCAG	1087	
QY	1081	AGATGAGGGGCCGTGAG	CGAGACACAGCAGCTTGTATCCCCAGCGACAGGAGGAGGACGAGG	1140	
D6	1088	AGATGAGGGGCCGTGAG	CGAGACACAGCAGCTTGTATCCCCAGCGACAGGAGGAGGACGAGG	1147	
QY	1141	AAGCTCCGGGGGAGGGAGAA	CCACAGAACTGAGAGAGAAAGTAGCTACACATCG	1200	
D6	1148	AAGCTCCGGGGGAGGGAGAA	CCACAGAACTGAGAGAGAAAGTAGCTACACATCG	1207	
QY	1201	ATGAAAAATGAAGCAGAA	TCTGACAGACAAACGACAGGCCCTGGAGGGGATGACAGAA	1260	
D6	1208	ATGAAAAATGAAGCAGAA	TCTGACAGACAAACGACAGGCCCTGGAGGGGATGACAGAA	1267	
QY	1261	ACATAGATGTTTTTAATGTT	GAAGATCAGAAAGAGACACCATTAATTTACTTGATCAGC	1320	
D6	1268	ACATAGATGTTTTTAATGTT	GAAGATCAGAAAGAGACACCATTAATTTACTTGATCAGC	1327	
QY	1321	GTGAAAAGCGGATCATAC	ACTCTGAATTTAGACTGGATCACATATTTACACACAGGGCC	1380	
D6	1328	GTGAAAAGCGGATCATAC	ACTCTGAATTTAGACTGGATCACATATTTACACACAGGGCC	1387	
QY	1381	GAAAGATGACTTTAAAT	TGTTTCAAGGAGTGAATCTGAAAACTGTGAATGTGACTA	1440	
D6	1388	GAAAGATGACTTTAAAT	TGTTTCAAGGAGTGAATCTGAAAACTGTGAATGTGACTA	1447	
QY	1441	AATTAATGTAGTCTG	AGAGATGATTTATGTGAATTTAGTATGCATTTGTGTAGGA	1500	
D6	1448	AATTAATGTAGTCTG	AGAGATGATTTATGTGAATTTAGTATGCATTTGTGTAGGA	1507	
QY	1501	AAATGGATGGTCTTTAA	ACAGCTTTTGGGGGTACTTTGGAGTGTCTAATAGGT	1559	
D6	1508	AAATGGATGGTCTTTAA	ACAGCTTTTGGGGGTACTTTGGAGTGTCTAATAGGT	1567	
QY	1560	GTCAATTTTGGTAGT	AGTATTTCTGAGAGGCTCAACCAAACTGGAAACATAGT	1619	
D6	1568	GTCAATTTTGGTAGT	AGTATTTCTGAGAGGCTCAACCAAACTGGAAACATAGT	1627	

QY 2580 TTGAGATGCTAAAGCCCAAGAGATCGTTTGAACCAACCCCTCTATTTCAGAGGGGAAAA 2639
D6 2587 TTGAGATGCTAAAGCCCAAGAGATCGTTTGAACCAACCCCTCTATTTCAGAGGGGAAAA 2646
QY 2640 TGGGGCTAGAGATGCTAGAGAGATCTAGCTGGTGGCTGGACCCCTGGCCCTCACACAGA 2699
D6 2647 TGGGGCTAGAGATGCTAGAGAGATCTAGCTGGTGGCTGGACCCCTGGCCCTCACACAGA 2706
QY 2700 CTCGGAGTAGCTGGAGCTACAGGACACAGTCACTGAAGAGGCGCTGTTTGAATTTCA 2759
D6 2707 CTCGGAGTAGCTGGAGCTACAGGACACAGTCACTGAAGAGGCGCTGTTTGAATTTCA 2766
QY 2760 CGTGGCACTCCAACTTAAACATTTCTCATATGATGATGCTTGTAGTCACTAAGGTAA 2819
D6 2767 CGTGGCACTCCAACTTAAACATTTCTCATATGATGATGCTTGTAGTCACTAAGGTAA 2826
QY 2820 CTTTCCACCCAGAAAGGCACTAGATAAATCTTAGAGTACTTCACTCACTCTCTAA 2879
D6 2827 CTTTCCACCCAGAAAGGCACTAGATAAATCTTAGAGTACTTCACTCACTCTCTAA 2886
QY 2880 GTCTCTTCCAGCTCACTTTGAGTCTCTCTGGGGTTGATAGAAATTTCTCTTCTTT 2939
D6 2887 GTCTCTTCCAGCTCACTTTGAGTCTCTCTGGGGTTGATAGAAATTTCTCTTCTTT 2946
QY 2940 CTCATAAAGTCTTATTCATCTCACTGATTTTAAATTTGACCATAGATTTGCTGAGATA 2999
D6 2947 CTCATAAAGTCTTATTCATCTCACTGATTTTAAATTTGACCATAGATTTGCTGAGATA 3006
QY 3000 AATATGTTCTGTTCACTT 3017
D6 3007 AATATGTTCTGTTCACTT 3024

RESULT 4
US-10-210-120-114
; Sequence 114, Application US/10210120
; Publication No. US2003017536A1
; GENERAL INFORMATION:
; APPLICANT: Chinnaiyan, Arul M.
; APPLICANT: Rubin, Mark A.
; APPLICANT: Sreekumar, Arur
; TITLE OF INVENTION: Expression Profile of Prostate Cancer
; FILE REFERENCE: US-07221
; CURRENT APPLICATION NUMBER: US/10/210,120
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 60/309,581
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: US 60/334,468
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 114
; LENGTH: 3042
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-210-120-114

Query Match 99.0%; Score 2987.6; DB 14; Length 3042;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3012; Conservative 0; Mismatches 4; Indels 2; Gaps 2;
QY 1 GCTGGGCGACGGGGGAGAGCGCGGAGAGCTGAGAGCGCGGGGAGAGCGACC 60

D6 8 GTTGGGCGACGGGGGAGAGCGCGGAGAGCTGAGAGCGCGGGGAGAGCGACC 67
QY 61 CGGGGGGCTCGTAGGGGGGGGGGGGATCCCGAGGTGGGGGGGGGGAGCGCTCGGAAAGAGA 120
D6 68 CGGGGGGCTCGTAGGGGGGGGGGGGATCCCGAGGTGGGGGGGGGGAGCGCTCGGAAAGAGA 127
QY 121 TTCTCAGGGCTGATTTTGGATGATGGGCTTGGGAAAGGGGGTGGGAGATGAGTCCG 180
D6 128 TTCTCAGGGCTGATTTTGGATGATGGGCTTGGGAAAGGGGGTGGGAGATGAGTCCG 187
QY 181 CGGGCTCGTAGGGGGGGGGCTGGTGGCTGATCATCGTCTTGGGCTTCAACTACTGGA 240
D6 188 CGGGCTCGTAGGGGGGGGGCTGGTGGCTGATCATCGTCTTGGGCTTCAACTACTGGA 247
QY 241 TTGGAGCTCCCGGAGCGGTGGACCTCCAGACACAGGATCATGGAGCTGGAGAGCGAGGTTC 300
D6 248 TTGGAGCTCCCGGAGCGGTGGACCTCCAGACACAGGATCATGGAGCTGGAGAGCGAGGTTC 307
QY 301 GAGGGGGCTGGAGAGAGAGGGGGGGTGGAGCTGAAGAGAGAGAGAGTTCAGGAGAGAGC 360
D6 308 GAGGGGGCTGGAGAGAGAGGGGGGGTGGAGCTGAAGAGAGAGAGAGTTCAGGAGAGAGC 367
QY 361 TGGAGAGAGAGGGGAGAGCGTTGACAAAATCCAGTCCAGGCCACAACTTCCAGCTGGAGA 420
D6 368 TGGAGAGAGAGGGGAGAGCGTTGACAAAATCCAGTCCAGGCCACAACTTCCAGCTGGAGA 427
QY 421 GGGTCAACAGCTGTACAGAGAGAGAGGGGGTGGTGGTGAATACATCACAGAGTG 480
D6 428 GGGTCAACAGCTGTACAGAGAGAGAGGGGGTGGTGGTGAATACATCACAGAGTG 487
QY 481 AGAGGGCTCATCCGAGTGTCTGCAGAGCGCTTAAAGAGCGCTGCAGAGGAGATTCAGGAGAGC 540
D6 488 AGAGGGCTCATCCGAGTGTCTGCAGAGCGCTTAAAGAGCGCTGCAGAGGAGATTCAGGAGAGC 547
QY 541 TGCAGAGAGATGTCTTCCAGTTTCAGAGAGACCAAGACCTGGAGAGAGATTTCTCT 600
D6 548 TGCAGAGAGATGTCTTCCAGTTTCAGAGAGACCAAGACCTGGAGAGAGATTTCTCT 607
QY 601 ACAGCTGAGCGAGTGCATCAATCAGATGAAGAGGTGAAGAGACATGTGAGAGAGCGAA 660
D6 608 ACAGCTGAGCGAGTGCATCAATCAGATGAAGAGGTGAAGAGACATGTGAGAGAGCGAA 667
QY 661 TAGAGAGGTCACTCAAAAGGGGAGTGAAGCTGTAGCTTCCAGAGACATGATGAAGAGCA 720
D6 668 TAGAGAGGTCACTCAAAAGGGGAGTGAAGCTGTAGCTTCCAGAGACATGATGAAGAGCA 727
QY 721 ACGACAGAGACAGCAGCTCCAGGCGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGG 750
D6 728 ACGACAGAGACAGCAGCTCCAGGCGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGG 757
QY 781 GCGTGCACACACAGAGGTGCACAGGAGAGGAGAGAGTGTGTTGTTAAGAGAGAGTCCG 840
D6 788 GCGTGCACACACAGAGGTGCACAGGAGAGGAGAGAGTGTGTTGTTAAGAGAGAGTCCG 847
QY 841 AGACACAGCGCGCGAGTCCGAGTGTGTTTGGATTCAAGAGAGACAGATTTGAGAGAGG 900
D6 848 AGACACAGCGCGCGAGTCCGAGTGTGTTTGGATTCAAGAGAGACAGATTTGAGAGAGG 907
QY 901 AAGCAATGAGATCCAGTGTGTTGATGAGAGAGCGCTCAGAGAGAGAGTCCGCGAGAGC 960
D6 908 AAGCAATGAGATCCAGTGTGTTGATGAGAGAGCGCTCAGAGAGAGAGTCCGCGAGAGC 967

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US-10-341-434-120
; Sequence 120, Application US/10341434
; Publication No. US20030215835A1
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; TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes
; FILE REFERENCE: 90 204 205 R1
; CURRENT APPLICATION NUMBER: US/10/341,434
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 60/346,164
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/346,119
; PRIOR FILING DATE: 2002-01-15
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; NAME/KEY: CDS
; LOCATION: (148)..(1350)
; OTHER INFORMATION:
US-10-341-434-120

Query Match 99.0%; Score 2987.6; DB 15; Length 3042;
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Qy 121 TTCTCAGCGCTGATTTTGAATGATGGGCTTGGGAAAGCGGCGGTGCGAGCATGAAGTGGC 180
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Qy 181 CGGCGCTCGTGTGGCGCGCGCTGGTGGCGCTGCAATCATGCTTTGGGCTTCAACTACTGGA 240
Db 188 CGGCGCTCGTGTGGCGCGCGCTGGTGGCGCTGCAATCATGCTTTGGGCTTCAACTACTGGA 247
Qy 241 TTGGAGCTCCCGGAGGCTGGAGCTTCAGACACGATCATGTAGCTGGAGGAGCGGCTCC 300
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Db 248 TTGGAGCTCCCGGAGGCTGGAGCTCCAGACACGCGATCATGAGCTGGAGGCGAGGCTCC 307
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Search completed: April 4, 2004, 00:36:45
Job time : 733.997 secs

OM nucleic - nucleic search, using sw model

Run on: April 3, 2004, 01:46:51 ; Search time 5104.23 Seconds
(without alignments)
17650.880 Million cell updates/sec

Title: US-10-030-269A-7
Perfect score: 3017
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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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14: gb_est5:*
15: em_estfun:*
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17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
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22: em_gss_man:*
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28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	123.6	40.0	1206	29	AY414699	Homo sapi
2	1032.6	34.2	1201	9	AL565763	AL565763
3	935.4	31.7	1201	13	EX447229	EX447229
4	946	31.4	1201	9	AL565250	AL565250
5	942.8	31.2	1039	9	AL525714	AL525714
6	936.6	31.0	1079	12	BM548257	BM548257
7	932.2	30.9	1201	9	AL535069	AL535069
8	922.8	30.6	1360	9	AL525765	AL525765
9	917	30.4	1201	9	AL548068	AL548068
10	903	29.9	1063	13	EX402100	EX402100
11	886.2	29.4	1058	12	BM554565	BM554565
12	867	28.7	1201	13	EX358371	EX358371
13	865.4	28.7	1201	13	EX447230	EX447230
14	855.4	28.6	1201	9	AL572881	AL572881
15	835.4	28.4	929	13	EX327028	EX327028
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17	834	27.6	913	13	HQ228135	HQ228135
18	826.2	27.4	935	13	HQ939789	HQ939789
19	822.4	27.3	1206	29	AY414700	AY414700
20	811	26.9	874	14	CA488004	CA488004
21	788	26.1	900	13	EX349102	EX349102
22	787.2	26.1	868	13	HQ219839	HQ219839
23	779.6	25.8	859	13	BQ425938	BQ425938
24	775	25.8	1123	12	BM925894	BM925894
25	772.2	25.8	1103	13	EX457488	EX457488
26	773.6	25.6	871	13	BQ718602	BQ718602
27	772.8	25.6	794	13	EU617401	EU617401
28	771.4	25.6	1201	9	AL533767	AL533767
29	770.8	25.5	801	12	BM977757	BM977757
30	770.2	25.5	793	12	BQ000396	BQ000396
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35	752.8	25.0	785	14	CA422153	CA422153
36	750.8	24.9	797	14	CA424517	CA424517
37	750.2	24.9	793	13	BQ774404	BQ774404
38	749.8	24.9	856	13	BQ426029	BQ426029
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44	712	23.6	712	14	CD671559	CD671559
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Search completed: April 3, 2004, 16:37:37
Job time : 5116.43 secs

OM nucleic - nucleic search, using sw model

Run on: April 3, 2004, 00:09:01 ; Search time 9047.21 Seconds
(without alignments)
16863.481 Million cell updates/sec

Title: US-i0-C30-269A-9
Perfect score: 3520
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 3470272 segs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: gb_in:**

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30: em_htg_hum:**

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33: em_htg_mus:**

34: em_htg_pln:**
35: em_htg_fod:**
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	3520	100.0	3520	6	BD123657 Secretary
4	3520	100.0	3520	9	AK075556 Homo sapi
5	3513.6	99.8	5233	9	AF152308 Homo sapi
6	3150.8	89.5	5257	9	AF152307 Homo sapi
7	3135.8	89.1	5254	9	AF152306 Homo sapi
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22	2311.2	65.7	5206	10	AY013763 Mus muscu
23	2308.4	65.6	5245	10	AY013762 Mus muscu
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25	2307	65.5	5230	10	AY013761 Mus muscu
26	2306.6	65.5	4568	10	AK129120 Mus muscu
27	2302	65.4	5254	10	AY013758 Mus muscu
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33	2279	64.7	5215	10	AY013765 Mus muscu
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35	2168.2	61.6	5299	9	AF152303 Homo sapi
36	2160	61.4	5431	9	AF152304 Homo sapi
37	2156.8	61.3	5686	9	BC063288 Homo sapi
38	2101.2	59.7	3748	6	AX098224 Sequence
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 Hayashi,K.
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 Helix Research Institute (JP)
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 ORIGIN

Query Match 100.0%; Score 3520; DS 6; Length 3520;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3520; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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ACCESSION	BD123657	BD123657	VERSION	BD123657.1	GI:233218602					
KEYWORDS	JP 2002017376-A/166.		ORGANISM	Homo sapiens (human)						
REFERENCE	Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.									
TITLE	Secretory protein or membrane protein									
JOURNAL	Patent: JP 2002017376-A 166 22-JAN-2002;									
COMMENT	HELIX RESEARCH INSTITUTE									
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3001	Db	ATGTAATTACTAAATAAATGATCTCTCTTCTCTCTCTCTCTCTTTTCTCTAGAACAA	3060
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RESULT 5			
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			linear
			FRI 22-JUL-1999

DEFINITION Homo sapiens protocadherin alpha 12 (PCDH-alpha12) mRNA, complete cds.

ACCESSION AF152308

VERSION AF152308.1 GI:5456901

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 5233)

AUTHORS Wu, Q. and Maniatis, T.

TITLE A striking organization of a large family of human neural cadherin-like cell adhesion genes

JOURNAL Cell 97 (6), 779-790 (1999)

MEDLINE 99386636

REFERENCE 2 (bases 1 to 5233)

AUTHORS Wu, Q. and Maniatis, T.

TITLE Human protocadherin genes

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 5233)

AUTHORS Wu, Q. and Maniatis, T.

TITLE Direct Submission

JOURNAL Submitted (17-MAY-1999) Department of Molecular and Cellular Biology, Harvard University, 7 Divinity Avenue, Cambridge, MA 02138, USA

FEATURES

source

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ORIGIN

Query Match 99.8%; Score 3513.6; DB 9; Length 5233;

Best Local Similarity 99.9%; Pred. No. 0;

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DB 1249 AGCGTGTGCGCTATAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1308

QY 361 GCGACGCTAGAGTGTCCGTGGAGTGGCCGAGCTGAACGCAATGCGCTGCGCTGCGG 420

DB 1309 GCGACGCTAGAGTGTCCGTGGAGTGGCCGAGCTGAACGCAATGCGCTGCGCTGCGG 1368

QY 421 CAGCCCGAGTACACAGTGTCTGTAAGGAGAAACAACCGCGCGGCTGCCACATCTTCA 480

DB 1369 CAGCCCGAGTACACAGTGTCTGTAAGGAGAAACAACCGCGCGGCTGCCACATCTTCA 1428

QY 481 GTGTGGCATGGACGCGACGCGACGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540

DB 1429 GTGTGGCATGGACGCGACGCGACGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1488

QY 541 CCGCGGCTGGGCGAGCACGCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600

DB 1489 CCGCGGCTGGGCGAGCACGCACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1548

QY 601 GTGTACGCTGTGACGCGCTAGACACGAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 660

DB 1549 GTGTACGCTGTGACGCGCTAGACACGAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 1608

QY 661 GCGCGGCTGCGCGGCTGTGCGCGCTCTGGGCGACCAAGTGAAGCTGCAAGTGTGCTGCTG 720

DB 1609 GCGCGGCTGCGCGGCTGTGCGCGCTCTGGGCGACCAAGTGAAGCTGCAAGTGTGCTGCTG 1668

QY 721 GACGAGAACGCAACGCGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780

DB 1669 GACGAGAACGCAACGCGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1728

QY 781 GTTAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840

DB 1729 GTTAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1788

QY 841 GTTAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900

DB 1789 GTTAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1848

14 1054.6 30.0 2574 7 ACC00400
 15 1052 29.9 3045 7 ACC00401
 c 16 1051.2 29.9 7893 5 AAF76447
 17 857.8 24.4 2360 5 AAS65427
 18 738.2 21.0 1047 6 ABQ16376
 c 19 738.2 21.0 1047 6 ABQ16377
 c 20 677.6 19.2 1228 6 ABQ16381
 c 21 677.6 19.2 1228 6 ABQ16380
 c 22 676.8 19.2 2884 5 ADB62335
 c 23 638 18.1 1047 6 ABQ16374
 c 24 638 18.1 1047 6 ABQ16375
 c 25 627.2 17.8 1057 6 ABQ16373
 c 26 627.2 17.8 1057 6 ABQ16372
 27 623.2 17.7 730 5 AAF94096
 28 622.8 17.7 1139 6 ABQ16400
 c 29 622.8 17.7 1139 6 ABQ16401
 c 30 606.8 17.2 1151 6 ABQ16404
 c 31 606.8 17.2 1151 6 ABQ16405
 c 32 601.2 17.1 1166 6 ABQ16421
 c 33 601.2 17.1 1166 6 ABQ16420
 c 34 594.4 16.9 1084 6 ABQ16392
 c 35 594.4 16.9 1084 6 ABQ16393
 c 36 584.8 16.6 1060 6 ABQ16389
 c 37 584.8 16.6 1060 6 ABQ16388
 c 38 565 16.1 1015 6 ABQ16412
 c 39 565 16.1 1015 6 ABQ16413
 c 40 559.2 15.9 974 6 ABQ16424
 c 41 559.2 15.9 974 6 ABQ16425
 c 42 553 15.7 1228 6 ABQ16379
 c 43 553 15.7 1228 6 ABQ16378
 c 44 534.2 15.2 950 6 ABQ16396
 c 45 534.2 15.2 950 6 ABQ16397

ALIGNMENTS

RESULT 1
 ID AAF29361 standard; DNA: 3520 BP.
 XX AC AAF29361;
 XX DT 20-APR-2001 (first entry)
 XX DE Amyloid-beta protein agglutination regulating factor DNA SEQ ID 9.
 XX KW Human; amyloid-beta protein agglutination regulating factor;
 XX RW Alzheimer's disease; ds.
 XX OS Homo sapiens.
 XX EN WO200104299-A1.
 XX PD 18-JAN-2001.
 XX PF 06-JUL-2000; 2000WO-JP004515.
 XX PR 08-JUL-1999; 95JP-00194179.
 XX PR 18-OCT-1999; 99JS-0159586P.
 XX PA (HELI-) HELIX RES INST.

PI Ota T, Isegai T, Nishikawa T, Kawai Y, Yamazaki M, Satoh S;
 PI Arakawa H, Morita M;
 XX WPI; 2001-138347/14.
 DR P-PSDB; AAB49771.
 DR Abc16377 Oligonuel
 XX Abc16381 Oligonuel
 PT Polynucleotide encoding Amyloid-beta protein agglutination-controlling
 factor, useful for inhibiting or promoting agglutination or sedimentation
 of amyloid-beta protein and in diagnosis and screening drugs for
 PT Alzheimer's disease.
 XX PS Claim 1; Page 58-63; 72pp; Japanese.
 XX CC This invention relates to polynucleotides AAF29357 - AAF29361 which
 CC encode proteins AAB49767 - AAB49771. The proteins inhibit or promote the
 CC agglutination of amyloid beta protein. The protein and polynucleotide
 CC sequences are useful in the diagnosis of Alzheimer's disease. They are
 CC also useful for screening drugs which are useful for treating Alzheimer's
 CC disease
 XX SQ Sequence 3520 BP; 871 A; 896 C; 901 G; 852 T; 0 U; 0 Other;

Query Match 100.0%; Score 3520; DB 4; Length 3520;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3520; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 1 GAATTCAGGTTAAGCCATGATGAAGGATTCCTCCATGGCAGTCAAGCATGGTC 60
 QY 61 CTGGTGAATCTGAGCTGATGACATGTCCTGAACTAAGTACTTCACTCTG 120
 Db 61 CTGGTGAATCTGAGCTGATGACATGTCCTGAACTAAGTACTTCACTCTG 120
 QY 121 CTCCTCTGCAAGAGGATGCTCAGTGGGTACCTGATCCCTGATTAGCGTTCGGAT 180
 Db 121 CTCCTCTGCAAGAGGATGCTCAGTGGGTACCTGATCCCTGATTAGCGTTCGGAT 180
 QY 181 CGTGACTCTGGACCAATGGACAGGTCATCTGCTCACTGACACCTCATGTCCTTCAAG 240
 Db 181 CGTGACTCTGGACCAATGGACAGGTCATCTGCTCACTGACACCTCATGTCCTTCAAG 240
 QY 241 CTGGTGTCCACCTACAGATTACTCTGTTGGTCTGGACAGCGCCCTGGACCGGAG 300
 Db 241 CTGGTGTCCACCTACAGATTACTCTGTTGGTCTGGACAGCGCCCTGGACCGGAG 300
 QY 301 AGCGTGTGGCCCTTATGAGCTGTTGTTGACTCGCGGGGATGGGGGCTGGCTTGG 360
 Db 301 AGCGTGTGGCCCTTATGAGCTGTTGTTGACTCGCGGGGATGGGGGCTGGCTTGG 360
 QY 361 GCCACGGCTAGAGTGTCCGTGGAGTGGCGGACGTGAACGACATGGCGTCCG 420
 Db 361 GCCACGGCTAGAGTGTCCGTGGAGTGGCGGACGTGAACGACATGGCGTCCG 420
 QY 421 CAGCCCGATACACAGTGTCTGTGAAGGAGAACACCGCCGGCTGCCACATCTCAAG 480
 Db 421 CAGCCCGATACACAGTGTCTGTGAAGGAGAACACCGCCGGCTGCCACATCTCAAG 480
 QY 481 GTGTGGGATGGGACGGGACGGCAGAAAGACGGCTGTCTACTCTGCTGGTGGAG 540
 Db 481 GTGTGGGATGGGACGGGACGGCAGAAAGACGGCTGTCTACTCTGCTGGTGGAG 540
 QY 541 CGCGGGTGGGCGAGCAGCACTGTGTGGAGCTAGTGTGCTGACGGGAGAGCGGAG 600

Qy	1501	GGCATCTACGGGCTGGTTCAGGAGGGCCGTGATCAGCAGTGGGCCAACAGTATCACTGCA	1560
Db	1501	GGCATCTACGGGCTGGTTCAGGAGGGCCGTGATCAGCAGTGGGCCAACAGTATCACTGCA	1560
Qy	1561	ACACACAGAACACAGCAGAGAGAAAGTGTCCCTCCAGTCCGGTGGGGGTGTCAACACAGAC	1620
Db	1561	ACACACAGAACACAGCAGAGAGAAAGTGTCCCTCCAGTCCGGTGGGGGTGTCAACACAGAC	1620
Qy	1621	AGCTGGACCTTTAAATAGCAGACAGGCAACCCCAAAACAATCCGGTCCCGGTGAGTTGCC	1680
Db	1621	AGCTGGACCTTTAAATAGCAGACAGGCAACCCCAAAACAATCCGGTCCCGGTGAGTTGCC	1680
Qy	1681	GACAAATTCATTAACCGAGATCTCTGCAATGATCTCCATCTGGCACAGAGGCTACTAAC	1740
Db	1681	GACAAATTCATTAACCGAGATCTCTGCAATGATCTCCATCTGGCACAGAGGCTACTAAC	1740
Qy	1741	AGCCAAATTCACAAAGTGACTTCATAACCTTGGCAAAAGGAGGAGACCCAGAAAG	1800
Db	1741	AGCCAAATTCACAAAGTGACTTCATAACCTTGGCAAAAGGAGGAGACCCAGAAAG	1800
Qy	1801	AAGAAAAAGAAAGAGGTTAACAGACCCAGAGAAAAAAGAAAGAGGGAACAGCAGACT	1860
Db	1801	AAGAAAAAGAAAGAGGTTAACAGACCCAGAGAAAAAAGAAAGAGGGAACAGCAGACT	1860
Qy	1861	GACACAGTGACCACTGAGGTCTCAATGGAAACAAGCCACTTAGCCAGTTTTCGTAAT	1920
Db	1861	GACACAGTGACCACTGAGGTCTCAATGGAAACAAGCCACTTAGCCAGTTTTCGTAAT	1920
Qy	1921	AATGGCAATCTCTCCCATGTAGCAATTCCTGCTCTTTTCTGATCTACACAGGCGCT	1980
Db	1921	AATGGCAATCTCTCCCATGTAGCAATTCCTGCTCTTTTCTGATCTACACAGGCGCT	1980
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Db	1981	CTTAGAGACCTTCAGAAATCTGCAGAAAGTTCCCTGTGTCTCTAGAACGCATTTAAG	2040
Qy	2041	GTTTTGTGTAAAGCTTACTAAGTGTGAGTTAACTCTTTCTCTCCACTCTGGCTGT	2100
Db	2041	GTTTTGTGTAAAGCTTACTAAGTGTGAGTTAACTCTTTCTCTCCACTCTGGCTGT	2100
Qy	2101	TTTCAGACCTTAAAGACAGACCCAGTTTCCTTCTCTCCGCGCAAGGAGAGGCTT	2160
Db	2101	TTTCAGACCTTAAAGACAGACCCAGTTTCCTTCTCTCCGCGCAAGGAGAGGCTT	2160
Qy	2161	CCACGCCCGCCAGTGAAGAGTTGAGACTCTGCGCTGTGTCCGGGATCCTGTCTTGA	2220
Db	2161	CCACGCCCGCCAGTGAAGAGTTGAGACTCTGCGCTGTGTCCGGGATCCTGTCTTGA	2220
Qy	2221	TGACACTTCAGGCGCAGCTGAAGAATTTGAGATTAGACAGCTTCGGAGTTTGGGCA	2280
Db	2221	TGACACTTCAGGCGCAGCTGAAGAATTTGAGATTAGACAGCTTCGGAGTTTGGGCA	2280
Qy	2281	CTGGGTGTGTAGCTACCGCGGGTATGCAGTGGCCAGATATGGCTTGAGACGAGCCAG	2340
Db	2281	CTGGGTGTGTAGCTACCGCGGGTATGCAGTGGCCAGATATGGCTTGAGACGAGCCAG	2340
Qy	2341	TTAGACTAATTTGGTACAGGAGGCCAGAAACAAGACAAATAAACAAGCGGAAGTTATC	2400
Db	2341	TTAGACTAATTTGGTACAGGAGGCCAGAAACAAGACAAATAAACAAGCGGAAGTTATC	2400
Qy	2401	AGTATGGAGGGAGGTGTAAACTTTAAAGGACCAAGCTTTTCTAAATCTTAACTCAAGA	2460
Db	2401	AGTATGGAGGGAGGTGTAAACTTTAAAGGACCAAGCTTTTCTAAATCTTAACTCAAGA	2460

QY	2461	GTTGGCAGCCACCTCTAGGAGCAAACTTACCCCACTGACAGGCTTTAGGAGACCT	2520
DB	2461	GGTGGCAGCCACCTCTAGGAGCAAACTACCCCACTGACAGGCTTTAGGAGACCT	2520
QY	2521	AAAGTCTGTTGGCTGTGACGTCAATATACCTTAAATCTGCATCACTAGCTGCAAGCCACA	2580
DB	2521	AAAGTCTGTTGGCTGTGACGTCAATATACCTTAAATCTGCACTACTGCAAGCCACA	2580
QY	2591	GTTCACTGTTTTAAGCAGAGACACCTGGGAAAGAGAGAGATCGATGTTTCCTA	2640
DB	2591	GTTCACTGTTTTAAGCAGAGACACCTGGGAAAGAGAGAGATCGATGTTTCCTA	2640
QY	2641	TACATGTCCTGTGCTCACTTATTAATAATCTTTTGACACATGTTTATGAAGGCC	2700
DB	2641	TACATGTCCTGTGCTCACTTATTAATAATCTTTTGACACATGTTTATGAAGGCC	2700
QY	2701	AGATCTCTTTCCAAATCAATGCAAAAGCAAAAGAAACCCGAGACTGACCTTCGCT	2760
DB	2701	AGATCTCTTTCCAAATCAATGCAAAAGCAAAAGAAACCCGAGACTGACCTTCGCT	2760
QY	2761	GTTTGTTGTTTCATAGATTTATTAATAAGAGAAAGTCTATAGCTATAATCTTTAA	2820
DB	2761	GTTTGTTGTTTCATAGATTTATTAATAAGAGAAAGTCTATAGCTATAATCTTTAA	2820
QY	2821	GGAAATATGAATCAATTCCTTAACTCTCTCAAAAGAGAAATCAGCTACAGCCT	2880
DB	2821	GAGAAATATGAATCAATTCCTTAACTCTCTCAAAAGAGAAATCAGCTACAGCCT	2880
QY	2881	TTAATGATCAATGCTGCTACAGAGTGCITTAAGAGAAATGCTGAAACATCTGTATTA	2940
DB	2881	TTAATGATCAATGCTGCTACAGAGTGCITTAAGAGAAATGCTGAAACATCTGTATTA	2940
QY	2941	TATGGCCACCTGCCAATCACAGCTTTACTCTTTCAGGTCACTCTGGGGTGCCTTTC	3000
DB	2941	TATGGCCACCTGCCAATCACAGCTTTACTCTTTCAGGTCACTCTGGGGTGCCTTTC	3000
QY	3001	ATGTATTACTAAATAAATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	3060
DB	3001	ATGTATTACTAAATAAATGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	3060
QY	3061	TTATGTGCACCTTGATACACACCTCTCTAACCACATATATCAAGCCCAAAATG	3120
DB	3061	TTATGTGCACCTTGATACACACCTCTCTAACCACATATATCAAGCCCAAAATG	3120
QY	3121	AAGAAAATATTTTTCTCATACGTGAGGGATTTTCAATCTACTATCTCTGACT	3180
DB	3121	AAGAAAATATTTTTCTCATACGTGAGGGATTTTCAATCTACTATCTCTGACT	3180
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QY	3301	CTGTATGCTATGCTAAGACTCCTGAAATATACTACTCTGTGTGTGTATGTGAATTT	3360
DB	3301	CTGTATGCTATGCTAAGACTCCTGAAATATACTACTCTGTGTGTGTATGTGAATTT	3360
QY	3361	ATTGCACTATTACCTAGAGTAACCTTAAGCTTTATTTGTGAATGTAATTCATATAT	3420

CC polypeptides may be used as antigens in the production of antibodies
CC against them and in assays to identify modulators (agonists and
CC antagonists) of expression and activity. The antibodies and antagonists
CC may also be used as therapeutic agents to down regulate expression and
CC activity. The antibodies may also be used as diagnostic agents for
CC detecting the presence of the polypeptides in samples (e.g. by enzyme
CC linked immunosorbent assay (ELISA)). Examples of diseases which may be
CC treated include rheumatoid arthritis and diabetes

XX
SQ Sequence 3520 BP; 871 A; 896 C; 901 G; 852 T; 0 U; 0 Other;
Query Match 100.0%; Score 3520; DB 5; Length 3520;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3520; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAGTTAAGCCATTGATTAAGGGATTCTTCCATGGCAGGTACACGATGGTC 60
DB 1 GAATTCAGTTAAGCCATTGATTAAGGGATTCTTCCATGGCAGGTACACGATGGTC 60
QY 61 CTGGTGGAAATTCGGACGTGAATGACAAATGTCCTGAATGATGTTACTTCACTGTG 120
DB 61 CTGGTGGAAATTCGGACGTGAATGACAAATGTCCTGAATGATGTTACTTCACTGTG 120
QY 121 CTCCTGTGCAAGAGGATGCTCAGGTGGGTACCGTCAATGCCCTGATTAGCGTGGAT 180
DB 121 CTCCTGTGCAAGAGGATGCTCAGGTGGGTACCGTCAATGCCCTGATTAGCGTGGAT 180
QY 181 CTTGACTCTGAGGCCAATGGACAGGTCACTCTGCTCATTGACACCTCAATGTTCCCTCAAG 240
DB 181 CTTGACTCTGAGGCCAATGGACAGGTCACTCTGCTCATTGACACCTCAATGTTCCCTCAAG 240
QY 241 CTGGTCTCACTACAGAAATTAATCTACTGTTGGTGGTGGACAGCGGCTGGACCGGAG 300
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QY 301 AGCGTGTGGGCTATGAGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 360
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QY 421 CAGCCCGAGTACACAGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 480
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QY 601 GTGTAGCGGCTGACGCGGCTAGACACGAGGAGTGGAGTGTGCTGCTGCTGCTGCTG 660
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QY 661 GCAGCGGACGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
DB 661 GCAGCGGACGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720

QY 721 GACGAGACGACAAACGCGCGGCACTGCTGGGCACTCGGCTGGCAAGGAGGAGGCA 780
DB 721 GACGAGACGACAAACGCGCGGCACTGCTGGGCACTCGGCTGGCAAGGAGGAGGCA 780
QY 781 GTTAGCGAGTGTGTAACCGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 840
DB 781 GTTAGCGAGTGTGTAACCGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 840
QY 841 GTGACGCTGACTTCCGGCTATAACGCTTGGCTGTCTAGAGTGTGCAACGCGGCGGCTC 900
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QY 1201 TTGTACTGCGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1260
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DB 1381 CAGCTGTCTCGAAGAGATTGTTAAATCCTCCAGTGAACACGACAGACGACGACGACGAC 1440
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[illegible]

OM nucleic - nucleic search, using sw model

Run on: April 3, 2004, 11:14:53 ; Search time 845.87 Seconds
 (without alignments)
 15564.412 Million cell updates/sec

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 Perfect score: 3520
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Scoring table: IDENTITY NJC
 Gapop 10.0 , Gapext 1.0

Searched: 2466186 seqs, 1870095128 residues

Total number of hits satisfying chosen parameters: 4932372

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published Applications NA:*

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- 18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB ID	Description
1	2101.2	59.7	3748	14	US-10-176-847-101	Sequence 101, App
2	1167.6	33.2	1356	9	US-09-764-870-86	Sequence 86, Appl
3	1167.6	33.2	1356	14	US-10-125-540-86	Sequence 86, Appl
4	1103.4	31.3	1105	14	US-10-029-386-22917	Sequence 22917, A
5	769.4	21.9	1037	14	US-10-029-386-22808	Sequence 22808, A

6 677.2 19.2 834 14 US-10-029-386-22888
c 7 676.8 19.2 2884 15 US-10-104-047-489
c 8 651.8 18.5 849 14 US-10-029-386-25221
c 9 570 16.2 570 14 US-10-029-386-3758
c 10 556 15.8 556 14 US-10-029-386-24103
c 11 551.4 15.7 553 14 US-10-029-386-9214
c 12 548 15.6 548 14 US-10-029-386-13109
c 13 538 15.3 720 14 US-10-029-386-20243
c 14 532 15.1 2894 15 US-10-161-493-119
c 15 512.4 14.6 514 14 US-10-029-386-10398
c 16 506 14.4 708 14 US-10-029-386-24195
c 17 503.8 14.4 591 14 US-10-029-386-2214
c 18 503.2 14.3 588 14 US-10-029-386-4336
c 19 501.6 14.3 577 14 US-10-029-386-11514
c 20 492 14.0 580 14 US-10-029-386-2131
c 21 489.6 13.9 547 9 US-09-864-761-7683
c 22 478.2 13.6 563 14 US-10-029-386-2659
c 23 473.2 13.4 550 14 US-10-029-386-2749
c 24 465.4 13.2 467 9 US-09-864-761-24387
c 25 462 13.1 574 14 US-10-029-386-2082
c 26 460 13.1 524 14 US-10-029-386-11711
c 27 449.2 12.8 518 14 US-10-029-386-6513
c 28 445.4 12.7 535 14 US-10-029-386-10495
c 29 444 12.6 557 14 US-10-029-386-10344
c 30 438.2 12.4 523 14 US-10-029-386-25028
c 31 437 12.4 589 9 US-09-864-761-7254
c 32 436 12.4 580 14 US-10-029-386-3754
c 33 434.8 12.4 559 14 US-10-029-386-24053
c 34 432.4 12.3 630 14 US-10-029-386-25414
c 35 422.2 12.0 571 14 US-10-029-386-9096
c 36 422 12.0 451 10 US-09-918-995-10991
c 37 415 11.8 415 14 US-10-029-386-17458
c 38 414.8 11.8 522 14 US-10-029-386-11315
c 39 413.8 11.8 420 10 US-09-960-706-107
c 40 411 11.7 452 10 US-09-918-995-13437
c 41 402.8 11.4 462 14 US-10-029-386-15914
c 42 391 11.1 533 9 US-09-864-761-12100
c 43 391 11.1 533 14 US-10-029-386-18264
c 44 376.8 10.7 547 14 US-10-029-386-3260
c 45 373 10.6 413 14 US-10-029-386-18036

Search completed: April 4, 2004, 00:36:51
Job time : 851.87 secs

Sequence 22888, A
Sequence 489, App
Sequence 25221, A
Sequence 3758, Ap
Sequence 24103, A
Sequence 9214, Ap
Sequence 13109, A
Sequence 10398, A
Sequence 10398, A
Sequence 24195, A
Sequence 2214, Ap
Sequence 4336, Ap
Sequence 11514, A
Sequence 2131, Ap
Sequence 7683, Ap
Sequence 2659, Ap
Sequence 2749, Ap
Sequence 24387, A
Sequence 2082, Ap
Sequence 11711, A
Sequence 6513, Ap
Sequence 10495, A
Sequence 10344, A
Sequence 25028, A
Sequence 7254, Ap
Sequence 3754, Ap
Sequence 24053, A
Sequence 25414, A
Sequence 9096, Ap
Sequence 10991, A
Sequence 17458, A
Sequence 11315, A
Sequence 107, App
Sequence 13437, A
Sequence 15914, A
Sequence 12100, A
Sequence 18264, A
Sequence 3260, Ap
Sequence 18036, A

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OM nucleic - nucleic search, using sw model

Run on: April 3, 2004, 01:46:51 ; Search time 5955.22 Seconds
(without alignments)
17650.880 Million cell updates/sec

Title: US-10-030-269A-9
Perfect score: 3520

Sequence: 1 gaaattcaggttaacgcoat.....taaaattttttttaaatac 3520

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST.*

1: em_estba.*
2: em_esthum.*
3: em_estin.*
4: em_estnu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_hico.*
9: gb_est1.*
10: gb_est2.*
11: gb_hic.*
12: gb_est4.*
13: gb_est5.*
14: gb_estfun.*
15: em_estfun.*
16: em_estom.*
17: em_gas_hum.*
18: em_gas_inv.*
19: em_gas_pln.*
20: em_gas_vrt.*
21: em_gas_fun.*
22: em_gas_mam.*
23: em_gas_mus.*
24: em_gas_pro.*
25: em_gas_fod.*
26: em_gas_phg.*
27: em_gss_vrt.*
28: gb_gss1.*
29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Query	Description
1	1356.2	38.5	2754	11	AK043822		AK043822 Mus muscu
2	1185.2	33.7	2891	11	BC030897		BC030897 Mus muscu
3	1177.2	33.4	2878	11	AK043725		AK043725 Mus muscu
4	875.2	24.9	2894	11	AK048990		AK048990 Mus muscu
5	864.2	24.6	917	13	BQ424699		BQ424699 AGENCOURT
6	746.6	21.2	839	12	BI831598		BI831598 603074629
7	745.4	21.2	773	12	BI753524		BI753524 603026670
8	736.4	20.9	739	14	CD239823		CD239823 FNPBVH12
9	716.4	20.4	912	9	AA626775		AA626775 ad09e07.s
10	703.4	20.0	763	10	BF983147		BF983147 602305866
11	698.4	19.8	720	14	CA436984		CA436984 UI-H-DF1-
12	697.4	19.8	703	12	BM685644		BM685644 UI-E-CIO-
13	637.6	18.1	847	10	BF793430		BF793430 602254901
14	626.4	17.8	678	12	BI850525		BI850525 imaagcc.1
15	591.8	16.8	957	13	BQ720698		BQ720698 AGENCOURT
16	575.4	16.3	584	13	BU071903		BU071903 im35g08.Y
17	566.4	16.1	575	13	BU071607		BU071607 im43b10.Y
18	551.4	15.7	554	9	AI268404		AI268404 qm05e10.x
19	545.2	15.5	749	12	BG709151		BG709151 602675025
20	536.6	15.2	787	13	BU750609		BU750609 CH3#034.E
21	528.8	15.0	736	12	BI602140		BI602140 603246261
22	523.6	15.0	562	28	AQ483592		AQ483592 RPCI-11-2
23	525.4	15.0	530	14	CB218096		CB218096 NISC.rb06
24	527.4	15.0	531	10	BE043069		BE043069 hc32e02.x
25	526.8	15.0	587	12	BG732993		BG732993 346670.MA
26	508.6	14.4	591	14	CA396936		CA396936 cs83r10.Y
27	506.4	14.4	828	14	CF537889		CF537889 UI-M-GIO-
28	501.8	14.3	711	12	BI599585		BI599585 603247760
29	499.4	14.2	636	10	BB641641		BB641641 BB641641
30	498.8	14.2	502	9	AI672463		AI672463 wa03e05.x
31	498	14.1	732	14	CE518847		CE518847 UI-M-GH3-
32	495.8	14.1	502	9	AA846453		AA846453 aj56b03.s
33	492.6	14.0	726	13	BQ191879		BQ191879 UI-R-DRI-
34	483	13.7	569	14	CE218095		CE218095 NISC.rb06
35	475.2	13.5	853	14	CD806992		CD806992 UI-M-GW0-
36	474.2	13.5	665	28	BZ203894		BZ203894 CH230-436
37	472.8	13.4	501	13	BQ639025		BQ639025 hd30e03.Y
38	472.8	13.4	970	13	BQ639025		BQ639025 AGENCOURT
39	462.4	13.1	970	13	BQ947259		BQ947259 AGENCOURT
40	457	13.0	681	13	BU280745		BU280745 603863621
41	453.4	12.9	843	13	RU249664		RU249664 603321109
42	452.4	12.9	455	9	AA973493		AA973493 oa45e05.s
43	452.4	12.9	455	10	AW162420		AW162420 au74e02.x
44	447.6	12.7	679	14	CF533624		CF533624 UI-M-GH0-
45	446.8	12.7	1019	12	BI465306		BI465306 603206625

Search completed: April 3, 2004, 16:37:45
 Job time : 5963.42 secs